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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:15:32 ; Search time 38 seconds
(without alignments)
1230.815 Million cell updates/sec

Title: US-09-944-807-2
Perfect score: 1817
Sequence: 1 METNFTPLNEVEVSYESA.....TNDTAANSASPPAETELQAM 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	351	AAU79035	Human formyl pepti
2	1811	99.7	351	AB856354	Non-endogenous hum
3	1244.5	68.5	350	AB856353	Non-endogenous hum
4	1157.5	63.7	343	AA021656	Mouse protein homo
5	1117	61.5	335	AA48713	G-protein coupled
6	1117	61.5	315	AA02685	G-protein coupled
7	554.5	30.5	356	AA090678	Human G protein-co
8	553.5	30.5	356	AA090683	Human mutant G pro
9	542.5	29.9	477	AAV72389	Mouse C3a receptor
10	542.5	29.9	477	AAU75166	Mouse anaphylatoxi

11	542	29.8	372	20	AAW86323	Kidney injury asso
12	509.5	28.0	482	18	AAW23367	Novel G-protein co
13	509.5	28.0	482	19	AAW42376	Homo sapiens C3a r
14	509.5	28.0	482	23	AAU99102	Human anaphylotoxi
15	508.5	28.0	482	17	AAW02151	Human G-protein co
16	508.5	28.0	482	18	AAW06540	C5a-like seven tra
17	508	28.0	355	22	AAW93557	Human polypeptide,
18	507	27.9	350	22	AB856337	Non-endogenous hum
19	507	27.9	363	22	AAW55822	Human bone marrow
20	507	27.9	363	22	AAW68196	Human bone marrow
21	507	27.9	363	22	AAW16016	Peptide #2454 enco
22	507	27.9	363	22	AAW28517	Peptide #2554 enco
23	506.5	27.9	482	22	AB856336	Non-endogenous hum
24	504.5	27.8	482	22	AB858339	Lung cancer associ
25	500	27.5	355	22	AAU01300	Human G-protein re
26	499.5	27.5	395	19	AAW44703	Human Th2/B19. Ho
27	499	27.5	355	21	AAW90609	Human G-protein re
28	497	27.5	355	22	AAU01299	Human G-protein re
29	497	27.4	355	21	AAW90643	Human mutant G pro
30	496	27.3	355	22	AAU01301	Human G-protein re
31	491	27.0	355	22	AAU01302	Human G-protein re
32	479	26.4	304	15	AAW48714	Human IL-8 recepto
33	479	26.4	304	17	AAW02686	G-protein coupled
34	431.5	23.7	360	16	AAW80953	Recombinant high a
35	430.5	23.7	1064	16	AAW70124	IL8-R type 2-GBP 1
36	428.5	23.6	355	23	AAU80485	Gorilla CXCR2 rece
37	427.5	23.5	360	23	AAU10558	Human interleukin
38	426.5	23.5	355	14	AAW33420	Human IL-8 recepto
39	426.5	23.5	355	17	AAW09990	Human IL-8 recepto
40	426.5	23.5	355	23	AAU80482	Human CXCR2 recept
41	426.5	23.5	355	23	AAU80483	Chimpanzee CXCR2 r
42	426.5	23.5	359	21	AAW02844	Human G protein co
43	426.5	23.5	359	23	AAO20951	Protein of the ang
44	426.5	23.5	359	23	AAU78654	Human Angiotensin
45	426.5	23.5	360	13	AAW28273	Sequence in a low

ALIGNMENTS

RESULT 1

AAU79035
ID AAU79035 standard; Protein; 351 AA.

AC AAU79035;

DT 18-JUN-2002 (first entry)

DE Human formyl peptide receptor like-1 receptor, FPRL-1.

XX Human; FPRL-1; formyl peptide receptor like-1; receptor;

KW ILM receptor; macrophage surface receptor; antiinflammatory; pulmonary;

KW chronic inflammatory airway disease; chronic bronchitis;

KW chronic obstructive pulmonary disease; COPD.

XX Homo sapiens.

XX WO200218938-A1.

PD 07-MAR-2002.

XX 23-AUG-2001; 2001WO-EP09727.

XX 01-SEP-2000; 2000GB-0021484.

XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.

PI Jung B, Kraut N, Mueller S, Kistler B, Seither P, Quast K;
Weith A;

XX WPI; 2002-315580/35.

DR N-PSDB; ABK48101.

XX

PT Determining an expression level of ILM (a macrophage surface receptor),
PT for the diagnosis or monitoring of chronic inflammatory airway disease,
PT comprises determining the level of the ILM receptor expressed in a
PT macrophage -

XX Claim 7; Page 49-51; 79pp; English.

PS The invention relates to determining an expression level of an ILM
PS receptor (macrophage surface receptor), comprises determining the level
PS of an ILM receptor expressed in a macrophage. Also included are a method
PS of determining whether a substance is an activator or an inhibitor of an
PS ILM receptor, involving applying the substance to a test system which
PS generates a measurable read-out upon modulation of the ILM receptor or an
PS ILM receptor function, a test system for determining whether a substance
PS is an activator or an inhibitor of an ILM receptor function,
PS characterised in that the receptor is involved in a chronic inflammatory
PS airway disease and where the receptor plays a role in mediating
PS inflammation comprising: (i) an ILM receptor; (ii) an expression vector
PS capable of expressing an ILM receptor in a cell; or (iii) a host cell
PS transformed with an expression vector capable of expressing the ILM
PS receptor and a substance determined to be an activator or inhibitor of an
PS ILM receptor. The methods are useful for the diagnosis or monitoring of a
PS chronic inflammatory airway disease, e.g. chronic bronchitis and chronic
PS obstructive pulmonary disease (COPD). The substance determined to
PS be an activator or inhibitor of an ILM receptor, is useful for treating
PS the diseases and for modulating an ILM receptor, in a macrophage.
PS The present sequence is an ILM receptor which is differentially
PS expressed and which is involved in causing the induction and/or
PS maintenance of the hyperactive status of macrophages involved in an
PS inflammatory process.

XX Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 23; Length 351;
Best Local Similarity 100.0%; Pred. No. 9.5e-196;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEEVEEYESAGYTVLRILPLVGLVTVFVGLVGLNGLVIVWAGFRMTRVT 60
DB 1 METNFTPLNEEVEEYESAGYTVLRILPLVGLVTVFVGLVGLNGLVIVWAGFRMTRVT 60
QY 61 TICYNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120
DB 61 TICYNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120
QY 121 LDRICVLHPVMAQNHRTVSLAMKVIVGVPWILALVLTLPVFLFTVTPNGDTCYCTNF 180
DB 121 LDRICVLHPVMAQNHRTVSLAMKVIVGVPWILALVLTLPVFLFTVTPNGDTCYCTNF 180
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKTHKGMKSSRPL 240
DB 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKTHKGMKSSRPL 240
QY 241 RVLTVAVASFFICWPFQVALLGVWVKEMLFYKGYKIIDLNVNPTSSLAFFNSCLNPM 300
DB 241 RVLTVAVASFFICWPFQVALLGVWVKEMLFYKGYKIIDLNVNPTSSLAFFNSCLNPM 300
QY 301 LYVFGQDFRERLIHSLPTSLSRALSEDSAPTNDTAANSASPPAETELQAM 351
DB 301 LYVFGQDFRERLIHSLPTSLSRALSEDSAPTNDTAANSASPPAETELQAM 351

RESULT 2
ABB56354

ID ABB56354 standard; Protein: 351 AA.

XX ABB56354;

XX 18-FEB-2002 (first entry)

XX Non-endogenous human GPCR protein, SEQ ID NO: 501.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;

KW constitutively activated GPCR; agonist; disease.

XX Homo sapiens.

OS Synthetic.

XX WO200177172-A2.

PN 18-OCT-2001.

PD 05-APR-2001; 2001WO-US11098.

XX 07-APR-2000; 2000US-195747P.

XX (AREN-) ARENA PHARM INC.

PA Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI: 2001-648759/74.

DR N-PSDB; ABI97990.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with
PT versions of GPCRs -

XX Claim 1; Page 301-302; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous
CC constitutively activated versions of known GPCRs are used in the
CC invention for the direct identification of candidate compounds as
CC receptor agonists, inverse agonists or partial agonists. Such
CC agonists are useful as therapeutic agents for diseases or disorders
CC associated with GPCRs. The present sequence is a non-endogenous
CC version of a known human GPCR.

XX Sequence 351 AA;

Query Match 99.7%; Score 1811; DB 22; Length 351;
Best Local Similarity 99.7%; Pred. No. 4.5e-195;
Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 METNFTPLNEEVEEYESAGYTVLRILPLVGLVTVFVGLVGLNGLVIVWAGFRMTRVT 60
DB 1 METNFTPLNEEVEEYESAGYTVLRILPLVGLVTVFVGLVGLNGLVIVWAGFRMTRVT 60
QY 61 TICYNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120
DB 61 TICYNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120
QY 121 LDRICVLHPVMAQNHRTVSLAMKVIVGVPWILALVLTLPVFLFTVTPNGDTCYCTNF 180
DB 121 LDRICVLHPVMAQNHRTVSLAMKVIVGVPWILALVLTLPVFLFTVTPNGDTCYCTNF 180
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKTHKGMKSSRPL 240
DB 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKTHKGMKSSRPL 240
QY 241 RVLTVAVASFFICWPFQVALLGVWVKEMLFYKGYKIIDLNVNPTSSLAFFNSCLNPM 300
DB 241 RVLTVAVASFFICWPFQVALLGVWVKEMLFYKGYKIIDLNVNPTSSLAFFNSCLNPM 300
QY 301 LYVFGQDFRERLIHSLPTSLSRALSEDSAPTNDTAANSASPPAETELQAM 351
DB 301 LYVFGQDFRERLIHSLPTSLSRALSEDSAPTNDTAANSASPPAETELQAM 351

RESULT 3

ABB56353

ID ABB56353 standard; Protein: 350 AA.

XX ABB56353;

XX 18-FEB-2002 (first entry)

XX Non-endogenous human GPCR protein, SEQ ID NO: 499.
DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease.
XX Homo sapiens.
OS Synthetic.
XX WO200177172-A2.
PN 18-OCT-2001.
XX 05-APR-2001; 2001WO-US11098.
PF 07-APR-2000; 2000US-195747P.
PR (AREN-) ARENA PHARM INC.
XX Lehmann-Brunisma K, Liaw CW, Lin I;
PI WPI; 2001-648759/74.
XX N-PSDB; ABI97989.
DR Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with
PT versions of GPCRs -
XX Claim 1; Page 299-300; 394pp; English.
XX The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous
CC constitutively activated versions of known GPCRs are used in the
CC invention for the direct identification of candidate compounds as
CC receptor agonists, inverse agonists or partial agonists. Such
CC agonists are useful as therapeutic agents for diseases or disorders
CC associated with GPCRs. The present sequence is a non-endogenous
CC version of a known human GPCR.
XX
XX Sequence 350 AA;
Query Match 68.5%; Score 1244.5; DB 22; Length 350;
Best Local Similarity 68.6%; Pred. No. 2.8e-131;
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;
QY 1 METNEFTPLNEYRVSYESAGTYVLRILPLVLGVTFVLGVGLVWAGFRMTRTFT 60
Db 1 METNSLPTNISGGTPAVSAGYLELDIITYLVFAVTFVLGVGLVWAGFRMTHVT 60
Y 61 TICVNLALADSFATLPLFLIVSWAMGEKPFQWFLCKLHIHVVDINLFGSVFLIGRIA 120
Db 61 TISYLNLAADFCFTSTLPLFFMVRKAMGGHPPFGWFLCKFTFTIVDINLFGSVFLIALIA 120
QY 121 LDRICVLHPVWQNHRTVSLAMKVIVGVPWILALVLTLPVLELTFTTTPNGDYCTENF 180
Db 121 LDRVCVLHPVWQNHRTVSLAMKVIVGVPWVALLLPLVIRTVTPGKTGTACTENF 180
QY 181 ASWGTPTPEERLKVATMLTARGIIRFVIGSLPMSIVAICYGLAAKHKKGMKSSRPL 240
Db 181 SPWTDNPKRINAVAMLTVRGIIRFVIGSAPMSIVAVSYGLIATKHKGLIKSSRPK 240
QY 241 RVLTAVASFFICWFPFOLVALLGKEMLFYKGYKIILVNPSSLAFFNSCLNPM 300
Db 241 RVLSEFAAFAFFLWSPYQVVALIATVRRELL-QGMKEIGIADVDTVSALAFFNSCLNPM 299
QY 301 LYVFGQDFRERLHSLTSLERALSSEDSAPTNDTAANSAPPAETELQA 350
Db 300 LYVFGQDFRERLHALPASLERALTEDSTQTSATNSTLPSAEVELQA 349

RESULT 4
AAO21656
ID AAO21656 standard; Protein; 343 AA.

XX AAO21656;
XX 05-SEP-2002 (first entry)
XX Mouse protein homologous to Mus musculus FMRL-3 protein.
XX Antibacterial; fungicide; protozoacide; virucide; anti-HIV; analgesic;
KW cytostatic; diabetes; anorectic; anabolic; antiasthmatic; cardiovascular;
KW antiparkinsonian; hypotensive; hypertensive; renal; antitumor; relaxant;
KW osteopathic; antianginal; antiischemic; antiallergic; antimigraine;
KW antiemetic; neuroprotective; tranquiliser; antischizophrenic; nootropic;
KW antidepressant; anticonvulsant; FMRL-3v; FMRL-3; HIV-1; HIV-2; pain;
KW cancer; diabetes; obesity; anorexia; bulimia; asthma; urinary retention;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer;
KW allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesias; gene therapy;
KW Huntington's disease; Gilles de la Tourette's syndrome; protein therapy;
XX vaccine; mouse; murine.
XX Mus musculus.
XX US2002045216-A1.
XX 18-APR-2002.
XX 12-JUN-2001; 2001US-0879017.
XX 12-JUN-2000; 2000US-210944P.
XX (ELSH/) ELSHOURBAGY N.
XX (LANE/) LANE P.
XX (TSUI/) TSUI P.
XX Eishourbagy N, Lane P, Tsui P;
XX WPI; 2002-507239/54.
XX N-PSDB; AAL39617.
XX Isolated polynucleotides encoding Mus Musculus FMRL-3v, useful for
PT identifying compounds for treating e.g. cancers, Parkinson's diseases
PT and depression -
XX Claim 4; Page 13; 16pp; English.
XX The invention relates to isolated polynucleotides encoding Mus Musculus
CC FMRL-3v proteins. The M. Musculus FMRL-3 polynucleotides and their vector
CC may be used in a process for producing the FMRL-3 polypeptides by
CC recombinant techniques in a host cell. The FMRL-3 polypeptides may be
CC used in assays for screening for compounds that either agonise or
CC antagonise M. Musculus FMRL-3. The compounds identified are useful in
CC the treatment of human diseases e.g. infections such as bacterial,
CC fungal, protozoan and viral infections (particularly infections by Human
CC immunodeficiency Virus (HIV)-1 or HIV-2), pain, cancers, diabetes,
CC obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart
CC failure, hypotension, hypertension, urinary retention, osteoporosis,
CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
CC prostatic hypertrophy; migraine, vomiting, psychotic and neurological
CC disorders (including anxiety, schizophrenia, manic depression,
CC depression, delirium, dementia, and severe mental retardation) and
CC dyskinesias (such as Huntington's disease or Gilles de la Tourette's
CC syndrome). The polynucleotides and proteins of the invention can be used
CC in the treating of disorders by gene therapy, protein therapy and
CC vaccination. This sequence represents a mouse protein with homology to
CC the Mus musculus FMRL-3 protein of the invention.
XX
XX Sequence 343 AA;

Query Match 63.7%; Score 1157.5; DB 23; Length 343;
Best Local Similarity 65.8%; Pred. No. 1.7e-121;
Matches 229; Conservative 39; Mismatches 75; Indels 5; Gaps 1;

QY 1 METNESTPLNEEVEYSAGYTVLRILPLVLGVTVFVLGNGLVIVWAGFRMTVT 60
 DB 1 MEANSIPLNGSEVFDSTTSRWILSVIVLSITFVLGNGLVIVWAGFRMAHTVT 60
 QY 61 TICYLNALADSFATLPFLIVSWAMGKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120
 DB 61 TICYLNALGDSFVWTLPLHIISWMGKWLFGFLCKFVLSVHINLFSVFLITLIA 120
 QY 121 LDRICVLPVWQNHRTVSLAMKIVGVPWILALVTLPLVFLELTVTTPNGDTCYTFNF 180
 DB 121 MDRCTCVLPVWQNHRTVSLARKVIVGAWILSLTLPLPFLFTTVRDARGEVHCTCNF 180
 QY 181 ASWGTPPEERLVAITMLTARGIIRVIGFSLPMSIVAIYGLIAAKIHKKGMIKSSRPL 240
 DB 181 ESWVNPPEQLKSVITVSTATGIISFIIGFSLPMSFVAVCYGLMAAKICRKGLNSSRPL 240
 QY 241 RVLTVAVASFFICWPFQVQVALLGVWVKEMLFYKIKYKIIDILVNTPTSSLAFFNSCLNPM 300
 DB 241 RVLTVAVASFFICWPFQVQVALLGVWVKEMLFYKIKYKIIDILVNTPTSSLAFFNSCLNPM 300
 QY 301 LVYVQGDPRKLIHSLPFLSRLSEDSAPTNDTAANSASPPAETEL 348
 DB 296 LVYVQGDPRKLIHSLPFLSRLSEDSAPTNDTAANSASPPAETEL 348

RESULT 5

AAW02685
 ID AAR48713 standard; Protein; 315 AA.

AC AAR48713;

DT 06-JUN-1996 (first entry)

DE G-protein coupled human N-formyl peptide receptor protein.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomagalovirus.

OS Homo sapiens.

PN W09405695-A1.

PD 17-MAR-1994.

PF 09-SEP-1993; 93WO-US08528.

PI 10-SEP-1992; 92US-0943236.

PA (UYNV) UNIV NEW YORK STATE.

PI Murphy RB, Schuster DI;

DR WPI; 1994-101120/12.

PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding

PS Disclosure; Page 87-88; 160pp; English.

CC Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
 CC of polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to

CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 SQ Sequence 315 AA;

Query Match 61.5%; Score 1117; DB 15; Length 315;
 Best Local Similarity 67.3%; Pred. No. 5.5e-117;

Matches 218; Conservative 37; Mismatches 59; Indels 10; Gaps 4;

QY 27 ILPLVLGVTVFVLGNGLVIVWAGFRMTVTTCYLNALADSFATLPFLIVSMA 86
 DB 1 IITLVFAVRFVLGNGLVIVWAGFRMTVTTCYLNALADSFATLPFLIVSMA 86
 QY 87 MGEKPPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRICVLPVWQNHRTVSLAMKVI 146
 DB 61 ---HWPFGLCKFLELTIVDINLFGSVFLIALDRICVLPVWQNHRTVSLAMKVI 117
 QY 147 VGPWILALVTLPLVFLELTVTTPNGDTCYTFNFASWGTPEERLVAITMLTARGIIRF 206
 DB 118 IGPWVWALLLPLVIRVTIVPGKGTGTVACITFNFSPWNPDKERINAVAMLTVRGIIRF 177
 QY 207 VIGFSLPMSIVAIYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWPFQVALLGTV 266
 DB 178 IIGFAPSMSIVAVSYGLIATKI-----IKSSRPLRVLSFVAAAFPLCWSYQVVALIATV 232
 QY 267 WLKEMLFYKIKYKIIDILVNTPTSSLAFFNSCLNPMILYVFGQDFRERLIHSLPFLSRLS 326
 DB 233 RIRELL-QGMYKEIGIADVDTSAIAFFNSCLNP-LYVFGQDFRERLIHALPASTLERALT 290
 QY 327 EDSAPTNDTAANSASPPAETELQA 350
 DB 291 EDSTOTSDTATNSTLPSAEVALQA 314

RESULT 6

AAW02685
 ID AAW02685 standard; peptide; 315 AA.

AC AAW02685;

DT 12-NOV-1996 (first entry)

DE G-protein coupled human N-formyl peptide receptor.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotonergic.

OS Homo sapiens.

PN US5508384-A.

PD 16-APR-1996.

PI 10-SEP-1992; 92US-0943236.

PR 09-SEP-1993; 93US-0118270.

PA (UYNV) UNIV NEW YORK STATE.

PI Murphy RB, Schuster DI;

DR WPI; 1996-208785/21.

PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia

PS Disclosure; Column 97-100; 184pp; English.

CC Proteins AAW02657-W02730 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,

Db 144 GCVWVAFVVCVFPVY-RDLFMDNRSICRYNFDSSRSYDWDYVYKLSLPESNSTNS 202
 Qy 183 -----WGCTPEE 189
 Db 203 TAQLTGHNDRSAPSSVQARDYFWVTVALQSOPFLTSPEDSFLDSANQQPHYGKPPN 262
 Qy 190 RLKVAI-----195
 Db 263 VLTAAVSGFPVEDRKSNLTNADAFLSAHTLFTPTASSGHLYPYDQGDYVDQFTYDNHV 322
 Qy 196 -TMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMKS-SRPLRLVLTAVVASFFIC 253
 Db 323 PTPLMAITITRLVGVGLVFPFFIWCYSLIVFRMKTFTKSRNKTFRVAVAVVTVFFIC 382
 Qy 254 WFPFQVALLGTWVWLKEMLFYGYKIIDLIVNPTSS-----LAFFNSCLNP 299
 Db 383 WTPYHLVG-----VLLITDPESSLGEAVMSWDHMSIALASANSFCNP 425
 Qy 300 MLYVFGQDFRERLIHSLTSLERALSSEDSAPTNDTAANSAS 341
 Db 426 FLYALLGKDFRKKARQSIKILEAAAFSELTHTSTNCTQDKAS 467
 RESULT 10
 ID AAU75166 standard; Protein; 477 AA.
 AC AAU75166;
 DT 08-MAY-2002 (first entry)
 DE Mouse anaphylatoxin C3a receptor.
 KW Mouse; transgenic; disruption of target gene; disease model;
 KW modulation of gene expression; behavioural phenotype; thymus abnormality;
 KW seizure; stimulus processing; anaphylatoxin C3a receptor; receptor.
 XX Mus musculus.
 XX WO200201950-A2.
 PD 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US20795.
 PR 29-JUN-2000; 2000US-215178P.
 PR 29-JUN-2000; 2000US-215179P.
 PR 29-JUN-2000; 2000US-215366P.
 PR 29-JUN-2000; 2000US-215402P.
 PR 29-JUN-2000; 2000US-215404P.
 PR 29-JUN-2000; 2000US-215466P.
 PR 27-JUL-2000; 2000US-215467P.
 PR 26-OCT-2000; 2000US-221667P.
 XX 26-OCT-2000; 2000US-244083P.
 FA (DELT-) DELTAGEN INC.
 XX Leviten MW, Brennan TJ, Guenther C, Klein R, Matthews W, Moore M;
 WPI: 2002-164479/21.
 DR N-PSDB; ABK13745.
 XX Novel transgenic mouse comprising disruption in target gene e.g., an
 PT anaphylatoxin C3a receptor gene, chordin gene, useful for identifying
 PT agents that modulate expression or function of target gene
 XX Disclosure; Fig 1; 90pp; English.
 XX The present invention relates to a method of creating transgenic animals,
 CC particularly transgenic mice, comprising a disruption in a target gene.
 CC Examples of target genes given in the specification include the mouse
 CC anaphylatoxin C3a receptor gene, 5-HT5A gene, chordin gene, RORgamma

CC gene, BMP gene, airway trypsin-like protease gene and the aquaporin
 CC gene. The transgenic mice are useful as models for disease and for
 CC identifying an agent that modulates the expression or function of a
 CC gene. The transgenic mice models are useful for identifying drugs and
 CC pharmaceutical therapies. They are also useful for testing and developing
 CC new treatments relating to behavioural phenotypes. They are useful for
 CC potential treatments for various diseases. For example, a transgenic
 CC mouse comprising a disruption in the anaphylatoxin C3a receptor gene is
 CC useful for identifying an agent that ameliorates a thymus abnormality,
 CC an increased susceptibility to seizure, or a stimulus processing deficit.
 CC The present sequence represents mouse anaphylatoxin C3a receptor. The
 CC encoding gene is disrupted to produce transgenic mice in the methods
 CC of the present invention.
 XX SQ Sequence 477 AA;
 Query Match 29.9%; Score 542.5; DB 23; Length 477;
 Best Local Similarity 28.1%; Pred. No. 4.8e-52;
 Matches 130; Conservative 58; Mismatches 109; Indels 165; Gaps 6;
 Qy 27 ILPLVVLGVTFVLGVLGVLVWAGFRMTRVTTTCYLNLAADFSTATPLPFLVMSA 86
 Db 24 IASMTLGLTCLLGLGLGVLWAGVKMTTNTVWFLHLTLADPLCCCLSLPFLSLAHLI 83
 Qy 87 MGEKWPFGHFLCKLHIVVDINLFGSVFLIGFALDRCICVLPWQAQHRVTSLAMKVI 146
 Db 84 LQGHWPYGLFLCKLIPSIILNMFASVFLTLAISLDRCLIVHKPIWQCNHRNVRTAFIC 143
 Qy 147 VGPWILALVLTLPVFLFTVTTPINGDTYCTFNFA-----182
 Db 144 GCVWVAFVVCVFPVY-RDLFMDNRSICRYNFDSSRSYDWDYVYKLSLPESNSTNS 202
 Qy 183 -----WGCTPEE 189
 Db 203 TAQLTGHNDRSAPSSVQARDYFWVTVALQSOPFLTSPEDSFLDSANQQPHYGKPPN 262
 Qy 190 RLKVAI-----195
 Db 263 VLTAAVSGFPVEDRKSNLTNADAFLSAHTLFTPTASSGHLYPYDQGDYVDQFTYDNHV 322
 Qy 196 -TMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMKS-SRPLRLVLTAVVASFFIC 253
 Db 323 PTPLMAITITRLVGVGLVFPFFIWCYSLIVFRMKTFTKSRNKTFRVAVAVVTVFFIC 382
 Qy 254 WFPFQVALLGTWVWLKEMLFYGYKIIDLIVNPTSS-----LAFFNSCLNP 299
 Db 383 WTPYHLVG-----VLLITDPESSLGEAVMSWDHMSIALASANSFCNP 425
 Qy 300 MLYVFGQDFRERLIHSLTSLERALSSEDSAPTNDTAANSAS 341
 Db 426 FLYALLGKDFRKKARQSIKILEAAAFSELTHTSTNCTQDKAS 467
 RESULT 11
 ID AAW86323 standard; Protein; 372 AA.
 AC AAW86323;
 DT 01-MAR-1999 (first entry)
 DE Kidney injury associated molecule HW055 protein.
 KW Kidney injury associated molecule; kidney injury related molecule;
 KW KIM; tissue growth promotion; regeneration; renal condition;
 KW acute renal failure; acute nephritis; tumour.
 XX Rattus sp.
 XX WO9853071-A1.
 XX 26-NOV-1998.
 PD 26-NOV-1998.
 XX

PF 22-MAY-1998; 98WO-US10547.
 XX 23-MAY-1997; 97US-0047491.
 PR 23-MAY-1997; 97US-0047490.
 XX (BIOJ) BIOGEN INC.
 XX Cate RL, Hession CA, Sanicola-Nadel M, Wei H;
 PI WPI; 1999-045312/04.
 XX N-PSDB; AAV80608.
 DR Kidney injury-associated molecule, KIM, polypeptides - upregulated
 DR in injured or regenerating tissues, useful to promote tissue growth
 DR and regeneration, especially to treat renal conditions
 XX Claim 17; Page 125-126; 213pp; English.
 XX The present sequence represents a kidney injury associated molecule
 CC (KIM) protein. KIM proteins can be administered therapeutically
 CC by expressing KIM encoding polynucleotides, to promote growth and/or
 CC survival of damaged tissue (e.g. renal tissue), since the KIM proteins
 CC are upregulated in injured or regenerating (especially renal) tissues.
 CC KIM fusion proteins, conjugates, antibodies and vectors can also be used
 CC therapeutically, e.g. these or the KIM proteins may be included with an
 CC acceptable carrier in pharmaceutical compositions, useful for therapy/
 CC prophylaxis of conditions associated with dysfunction/disregulation of
 CC KIM genes or proteins, especially renal diseases or impairments of renal
 CC function in humans (e.g. acute renal failure, acute nephritis). The
 CC polynucleotides can be used to produce antisense sequences which, when
 CC internalised into cells, can disrupt expression of a cellular KIM gene,
 CC also useful in therapy (e.g. to block the growth of tumours dependent on
 CC KIM for growth) or compositions. The proteins and polynucleotides are
 CC useful diagnostically e.g. to detect and quantify renal injury/disease
 CC (indicative of increased risk, or presence of, renal injury or impaired
 CC function), or abnormal responses to tissue injury (indicative of
 CC increased risk, or presence of, an autoimmune response or abnormal
 CC tissue growth arising from/affecting renal tissue). The proteins can
 CC also be used to locate KIM-producing cells (especially specific loci,
 CC e.g. tissue masses abnormally producing/expressing KIM such as tumours
 CC arising from/affecting renal tissue), by contacting cells with an
 CC imageable KIM-binding reagent and imaging reagent accumulation.
 XX Sequence 372 AA;
 SQ Query Match 29.8%; Score 542; DB 20; Length 372;
 Best Local Similarity 35.5%; Pred. No. 3.9e-52;
 Matches 123; Conservative 66; Mismatches 119; Indels 38; Gaps 8;
 11 EYEE-----VSTESAG---YTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTVTVTI 62
 15 EYSDGSDYIVDLEAGPLEAKVAEFLVVIYSLVCFGLTGLNGLVIATFRMKTNTV 74
 63 CYLNLALADFSATLPLFLIVSMACKWPGFGLCKLHIVVDLNFCSVFLGFIADL 122
 75 WFNVLAVDFLEIFLPIHITTAAMDYHWFGKAMCKISSFLSHNMVTSVFLLVISPD 134
 123 RCICVLHPVWQNHRTSVSLAMKVIWGPWTILALVLTLPVFLFTTVPNGDYCYCFNFAS 182
 135 RCISVLLPWQSNHRSVRSLAYWTCVWVWVLAFLSPSLVFRDVTSTSGKITCFNFSL 194
 183 WCGTPEE-----RLKVAITMLTARGIIRFVIGFSLPMSIYCAICYIAUKI 228
 195 ---AAPEPESHSTHPTDPVGYSRHVAVT-----VTRFLCGFLPIPVFIITACVLTIVFKL 246
 229 HKGMIKSRRLRLVLTAVVASFICWFFPOLVALLGTWVKEMLYGKYKIIDLVPNT 287
 247 QNRRLAKTKPKPKIITITITIFLCWCPVH-----TYLLELHHTVAPSVFSLGLPLA 300
 288 SSLAFNCSLNPMLVVFVGQDFRERLIHSLPTSLERALSSEDAPT 333
 301 TAVATANSNMNPLVFMGHDPKFKV-ALFSLRYNALSEDGPPS 345

RESULT 12
 AAW23367
 ID AAW23367 standard; Protein; 482 AA.
 XX
 AC AAW23367;
 XX
 DT 30-MAR-1998 (first entry)
 XX
 DE Novel G-protein coupled receptor with an enlarged extracellular domain.
 XX
 KW G-protein coupled receptor; enlarged extracellular loop;
 KW inflammatory disease; asthma; chronic obstructive pulmonary disease;
 KW cystic fibrosis; multiple sclerosis; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 9
 FT Domain /note= "predicted N-glycosylation site"
 FT Domain 22..160
 FT Domain /note= "putative transmembrane domain"
 FT Domain 163..327
 FT Modified-site /note= "enlarged extracellular loop"
 FT Domain 194
 FT Domain /note= "predicted N-glycosylation site"
 FT Domain 333..439
 FT Domain /note= "putative transmembrane domain"
 XX
 PN WO9728188-A1.
 XX
 PD 07-AUG-1997.
 XX
 PF 30-JAN-1997; 97WO-US01736.
 XX
 PR 30-JAN-1996; 96US-0010808.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Ye RD;
 XX
 DR WPI; 1997-402552/37.
 DR N-PSDB; AAT64946.
 XX
 PT G-protein-coupled receptor with enlarged extracellular domain -
 PT between fourth and fifth transmembrane domains, also nucleic acid
 PT and antibodies useful for treating inflammation and neurological
 PT disease
 XX
 PS Claim 4; Fig 1; 54pp; English.
 XX
 CC The present sequence represents a novel G-protein coupled receptor
 CC that has an enlarged extracellular loop between the fourth and fifth
 CC transmembrane domains. Antibodies generated against the present
 CC protein revealed expression in a variety of tissues, including
 CC heart, lung and placenta. Diseases or conditions mediated by the
 CC G-protein coupled receptor can be treated by administering reagents such
 CC as the present sequence, antisense nucleic acid or antibodies generated
 CC against the receptor. Reagents may comprise a molecule binding to the
 CC receptor but not transmitting a signal across the cell membrane or
 CC reducing effectiveness of binding of the natural ligand. The reagent may
 CC also alter the interaction of the receptor with the G-protein with which
 CC it naturally reacts e.g. by altering phosphorylation sites in
 CC intracellular domains of the receptor. Inflammatory diseases or
 CC conditions mediated by the novel receptor which can be treated include
 CC e.g. asthma, chronic obstructive pulmonary disease, cystic fibrosis,
 CC multiple sclerosis. The antibody can also be used to diagnose these
 CC diseases e.g. in brain tissue from patients with suspected neurological
 CC disease, especially Alzheimer's, in skin samples especially from patients
 CC with a suspected inflammatory disease or in haematopoietic cells. The
 CC nucleic acids are also useful in screening for compounds modulating gene
 CC expression by standard assays.
 XX

SQ Sequence 482 AA;

Query Match 28.0%; Score 509.5; DB 18; Length 482;
 Best Local Similarity 26.6%; Pred. No. 2.5e-48;
 Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 ETN----FSTPLNEYEVESAGYTVLRILPLVLGVGTVFVLGVLGNGLVWAGFRMTR 57
 DB 7 ETNSTDLLSQWNEPPV-----ILSMVLSITFLGPGNGLVWAGLKMQR 54

QY 58 TVTTCYLNALADFSFTATLPFLIVSMAMGEKWPFGFLCKLIHVVDINLFGSVFLIG 117
 DB 55 TVNTIWFHLTLADLLCLSLPFSLAHLAQGWPGYRFLCKLIPSIIVLNMFAVFLLT 114

QY 118 FIALDRICVLHPVMAQNHRTVSLAMKVIIVGVPWILALVLPVPLEFTTVTIPNGDYCT 177
 DB 115 AISLDRCLVVFKEPIWQNHNRVGMACSGCIIWVAVFVVCIPVYREIFTTDNHNR-CG 173

QY 178 FNFA-----SW-----183
 DB 174 YKFGLSLLDPDFYGDPLENRSLENIQVRGEMNDRLDPSSFTNDHPVTPTVFQPT 233

QY 184 -----GGTPEE-----190
 DB 234 FQPSADSLPRGSARLTSONLYSNVFKPADVVPKIPSPGPIEDHETSPLDNSDAFLSTH 293

QY 191 LKV-----ATMLTARGIIRFVIGFSLPMSIVA 218
 DB 294 LKLPSSASSNFYSELPQGFQDYINLQFTDDQVPTPLVAITITRLVVGFLLESVIMI 353

QY 219 ICYGLIAAKIHKGMKIS-SRPLRLVLTAVASFFTCFPFVALLGTVLWVKEMLFYGY 277
 DB 354 ACYSFIVFMQGRFAKQSKTFRVAVVVAVFLVCWTPYHI-----F 396

QY 278 KIIDLNVNPTS-----SLAFFNSCLNPMLYVFGQDFRERLIHSLPTSLSR 323
 DB 397 GVLSLLTDPETPLGKTLMSWDHVCIALASANSFCNPFYALLGDKFRKARQSIQIGILEA 456

QY 324 ALSDE-----SAPNDTAANSAS 341
 DB 457 AFSEELRSTRCHPSNNVISERN 479

RESULT 13
 AAW42376
 ID AAW42376 standard; Protein; 482 AA.
 XX AC AAW42376;
 XX 08-JUN-1998 (first entry)
 XX Homo sapiens C3a receptor.
 XX C3a receptor; treatment; diagnosis; atherosclerosis; chronic;
 KW polyarthritis; systemic vasculitis; multiple sclerosis; Alzheimer's;
 KW disease; acute inflammatory disease; Crohn's disease; food;
 KW allergies; non-bronchial allergies; osteoarthritis; osteoporosis;
 KW thyroid disease; coronary heart disease.
 XX OS Homo sapiens.
 XX PN EP814158-A2.
 XX 29-DEC-1997.
 XX 17-JUN-1997; 97EP-0304250.
 XX 17-JUN-1996; 96US-0019627.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Ames RS, Bergsma DJ, Foley JJ, Kumar C, Sarau HM;

DR WPI: 1998-044336/05.
 XX N-PSDB; AAV03250.
 PT C3a receptor agonists, antibodies and antagonists - useful for
 PT diagnosis of disease related to expression of C3a receptor, e.g.
 PT acute inflammatory disease, atherosclerosis, chronic polyarthritis,
 PT etc.
 XX Disclosure; Fig 1; 43pp; English.
 PS

The sequence is that of the C3a receptor. It can be used in a process for diagnosing a disease or susceptibility to a disease related to expression of the C3a receptor. This process involves analysing for the presence of a the C3a receptor in a sample derived from a patient suspected of having such a disease. C3a receptor-related diseases that can be detected by this method comprise acute inflammatory disease, atherosclerosis, chronic polyarthritis, systemic vasculitis, multiple sclerosis, Alzheimer's Disease, CNS inflammatory disease, Crohn's Disease, food allergies, non-bronchial allergies, osteoarthritis, osteoporosis, thyroid disease, coronary heart disease, Systemic Lupus Erythematosus SLE-associated nephritis, membranoproliferative GN, membranous nephritis, rheumatoid arthritis, Behcet's syndrome, juvenile rheumatoid arthritis, Sjogren's syndrome, myasthenia gravis, cerebellar lupus, Guillain-Barre syndrome, pemphigus/pemphigoid, phototoxic reactions, vasculitis, post-bypass syndrome, catheter reactions, sepsis, ARDS, anaphylaxis, transplant rejection, pre-eclampsia, atheroma, bowel inflammation, thyroiditis, infertility, susceptibility to pyogenic infections, glomerulonephritis, susceptibility to neisserial infections, recurrent subcutaneous swelling and mucosal oedema, and recurrent episodes of thrombosis/haemolysis. C3a receptor agonists, antagonists and antibodies can be used in the treatment of patients having need to inhibit or activate a C3a receptor.

XX SQ Sequence 482 AA;

Query Match 28.0%; Score 509.5; DB 19; Length 482;
 Best Local Similarity 26.6%; Pred. No. 2.5e-48;
 Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 ETN----FSTPLNEYEVESAGYTVLRILPLVLGVGTVFVLGVLGNGLVWAGFRMTR 57
 DB 7 ETNSTDLLSQWNEPPV-----ILSMVLSITFLGPGNGLVWAGLKMQR 54

QY 58 TVTTCYLNALADFSFTATLPFLIVSMAMGEKWPFGFLCKLIHVVDINLFGSVFLIG 117
 DB 55 TVNTIWFHLTLADLLCLSLPFSLAHLAQGWPGYRFLCKLIPSIIVLNMFAVFLLT 114

QY 118 FIALDRICVLHPVMAQNHRTVSLAMKVIIVGVPWILALVLPVPLEFTTVTIPNGDYCT 177
 DB 115 AISLDRCLVVFKEPIWQNHNRVGMACSGCIIWVAVFVVCIPVYREIFTTDNHNR-CG 173

QY 178 FNFA-----SW-----183
 DB 174 YKFGLSLLDPDFYGDPLENRSLENIQVRGEMNDRLDPSSFTNDHPVTPTVFQPT 233

QY 184 -----GGTPEE-----190
 DB 234 FQPSADSLPRGSARLTSONLYSNVFKPADVVPKIPSPGPIEDHETSPLDNSDAFLSTH 293

QY 191 LKV-----ATMLTARGIIRFVIGFSLPMSIVA 218
 DB 294 LKLPSSASSNFYSELPQGFQDYINLQFTDDQVPTPLVAITITRLVVGFLLESVIMI 353

QY 219 ICYGLIAAKIHKGMKIS-SRPLRLVLTAVASFFTCFPFVALLGTVLWVKEMLFYGY 277
 DB 354 ACYSFIVFMQGRFAKQSKTFRVAVVVAVFLVCWTPYHI-----F 396

QY 278 KIIDLNVNPTS-----SLAFFNSCLNPMLYVFGQDFRERLIHSLPTSLSR 323
 DB 397 GVLSLLTDPETPLGKTLMSWDHVCIALASANSFCNPFYALLGDKFRKARQSIQIGILEA 456

QY 324 ALSDE-----SAPNDTAANSAS 341
 DB 457 AFSEELRSTRCHPSNNVISERN 479

Db 457 AFSEELTRTHCPSNNVISERNS 479

RESULT 14

AAU99102
AAU99102 standard; Protein; 482 AA.

XX AAU99102;

DT 04-SEP-2002 (first entry)

XX Human anaphylotoxin C3a receptor.

XX Human; C3a; receptor; nootropic; neuroprotective; antiparkinsonian;
KW G protein-coupled receptor; GPCR; anaphylotoxin C3a receptor; AR;
KW Alzheimer's disease; Parkinson's disease; cell signalling; proliferation;
KW differentiation; leukocyte migration; gene transcription; vision; smell;
KW neurotransmission; hormonal response; ulcerative colitis; diabetes;
KW myocardial infarction; hypertension; asthma; bronchitis; pneumonia;
KW Crohn's disease; rheumatoid arthritis; Hodgkin's disease; glioblastoma;
KW neurodegenerative disorder.

OS Homo sapiens.

PN WO200244737-A2.

XX 06-JUN-2002.

PD 29-NOV-2001; 2001WO-US45220.

XX 29-NOV-2000; 2000US-250251P.

PR 30-NOV-2000; 2000US-250452P.

PR 17-OCT-2001; 2001US-330036P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Brown JP, Burmer GC, Roush CL, Morningstar DA;

DR WPI; 2002-508526/54.

DR N-PSDB; ABK86860.

XX Isolated and purified composition useful for manufacture of medicament

XX for inhibiting, preventing or treating Alzheimer's or Parkinson's

XX disease, comprises G protein-coupled receptor anaphylotoxin C3a

XX receptor

XX Disclosure; Fig 1; 112pp; English.

XX The invention discloses an isolated and purified composition including
XX the G protein-coupled receptor (GPCR) anaphylotoxin C3a receptor (AR) and
XX a pharmaceutically acceptable carrier for use in the manufacture of a
XX medicament for inhibiting, preventing or treating Alzheimer's disease or
XX Parkinson's disease. G protein-coupled receptors are involved in cell
XX signalling and play key roles in cell proliferation, differentiation,
XX leukocyte migration, gene transcription, vision, smell, neurotransmission
XX and hormonal response. Compositions relating to the anaphylotoxin C3a
XX receptor can also be used against ulcerative colitis, diabetes,
XX myocardial infarction, hypertension, asthma, bronchitis, pneumonia,
XX Crohn's disease, rheumatoid arthritis, Hodgkin's lymphoma, glioblastomas
XX and other neurodegenerative disorders. The compositions include
XX antibodies, agonists, antagonists, probes, antisense and gene therapies.
XX The anaphylotoxin C3a receptor sequence can be used to manufacture
XX medicaments able to reduce symptoms associated with Alzheimer's or
XX Parkinson's disease in a human patient, by combining a pharmaceutically
XX effective amount of an AR agonist or antagonist, a pharmaceutically
XX acceptable carrier, adjuvant, excipient, buffer and diluent, and for
XX detecting an increased possibility of Alzheimer's or Parkinson's disease.
XX The sequence presented is the human anaphylotoxin C3a receptor.

XX Sequence 482 AA;

XX Query Match

XX Best Local Similarity 28.0%; Score 509.5; DB 23; Length 482;

XX 26.6%; Pred. No. 2.5e-46;

Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 ETN----FSTPLNEYEEVSEYAGYTVLRILPLVLGVTFVLGVLGNGLVIVWAGFRMTR 57
DB 7 ETNSTDLLSQPNPEPV-----ILSNVILSLTFLGLGPNGLVWAGLKMQR 54
QY 58 TVTTTCYLNALADFSFTATLPFLIVSMAMGEKWPGEWFLCKLHIHIVDINLFGSVFLIG 117
DB 55 TVNTTWFLTLTADLCLCLSLPFLSLAHLALOGOWPYGREFLCKLIPSIIVLNMFASVFLLT 114
QY 118 ETALDRICVLPVMAONHRTVSLAMKVIVGWPILALVLTLPVFLFTTTPNGDTYCT 177
DB 115 ALSLDRCLVVFPIWQNHNRNVMGACSGCIWVAVFVVCIPVFVYREIFTTDNHNR-CG 173
QY 178 FNFA-----SW-----183
DB 174 YKFGLSLSDYDFYCDPLENLSLENIQPPGEMNDRLDPSSFQINDHPWTVTVPQPT 233
QY 184 -----GTPPE-----R 190
DB 234 FORPSADSLPRGSARLTSONLYSNVFKPADVVSPPKIPSGFPIEDHETSPLDNSDAFLSTH 293
QY 191 LKV-----AITMLTARGIIRFVIGSLPMSIVA 218
DB 294 LKLFPSASSNSYESELPGQFQDYNNLGFTDDQVPTFLVAITITRLVYVGLLPSVIMI 353
QY 219 ICYGLIAAKHKGMKS-SRPLRLVLTAVVASFFICWFQFQVALLGLTVLWLEMLFYGVY 277
DB 354 ACYSFIVFMQGRFAKSKQSTFRVAVVVAVFLVCWTEYHI-----F 396
QY 278 KIIDLNVPTS-----SLAFFNSCLNPMLYVFGQDFRERLIHSLPISLER 323
DB 397 GVLSSLTDPETPLGKTLMSWDHVCIALASANSFCNPFYALLGLKDFKRKARQSIQGLEA 456
QY 324 ALSLED-----SAPTNDTAANSAS 341
DB 457 AFSEELTRTHCPSNNVISERNS 479

RESULT 15

AAW02151
ID AAW02151 standard; Protein; 482 AA.

XX AC AAW02151;

XX 08-DEC-1996 (first entry)

XX Human G-protein coupled receptor.

XX G-coupled receptor; asthma; transplant rejection; immunodeficiency;
XX severe infection; membrane protein.

XX Homo sapiens.

XX WO9625432-A1.

XX 22-AUG-1996.

XX 17-FEB-1995; 95WO-US01992.

XX 17-FEB-1995; 95WO-US01992.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Rosen CA;

XX WPI; 1996-393343/39.

XX DR N-PSDB; AAT36375.

XX DNA encoding G-protein coupled receptor - and antagonists and
XX agonists, useful to treat asthma and transplant rejection, and
XX immunodeficiency and severe infections, respectively

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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:17:27 : Search time 20 Seconds
(without alignments)
1687.159 Million cell updates/sec

Title: US-09-944-807-2
Perfect score: 1817
Sequence: 1 MEINFSPLENEYEVSYESA.....TNDTAANSAPPAETELQAM 351

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	351	2 B42009	FMLP-related recep
2	1318	72.5	353	2 C42009	FMLP-related recep
3	1249.5	68.8	350	2 A42009	N-formyl peptide I
4	1223.5	67.3	352	2 A46520	N-formyl peptide I
5	1174.5	64.6	364	2 A49542	N-formyl peptide C
6	538.5	29.6	371	2 JC5498	G protein-coupled
7	530.5	29.2	473	2 JC5835	anaphylatoxin C3a
8	513	28.2	350	1 A37963	complement C5a ana
9	509.5	28.0	482	2 S65766	G protein-coupled
10	502.5	27.7	371	2 JC5796	probable chemoattr
11	502	27.6	353	2 JC2492	G protein-coupled
12	500	27.5	352	1 S27357	complement C5a ana
13	499	27.5	355	2 A55733	G protein-coupled
14	457.5	25.2	351	1 A46525	complement C5a ana
15	430.5	23.7	359	2 JC2134	angiotensin II rec
16	427.5	23.5	359	2 JH0621	angiotensin II rec
17	426.5	23.5	359	2 JC1104	angiotensin II rec
18	426.5	23.5	360	2 A53611	interleukin-8 rece
19	423.5	23.3	359	2 S15403	angiotensin II rec
20	422.5	23.3	355	2 JQ1231	interleukin-8 rece
21	420.5	23.1	359	2 A42656	angiotensin II rec
22	420.5	23.1	359	2 JQ1516	angiotensin II rec
23	419.5	23.1	352	2 A45747	neuropeptide Y/pep
24	418.5	23.0	359	2 A48857	angiotensin II rec
25	418.5	23.0	359	2 J39418	angiotensin II rec
26	418	23.0	359	2 S44425	angiotensin II rec
27	413.5	22.8	352	2 G00048	fusin (LESTRA) - C
28	413.5	22.8	359	2 JC1194	angiotensin II rec
29	412	22.7	362	2 A30341	G protein-coupled

30	411.5	22.6	353	2 S28787	neuropeptide Y/pep
31	411.5	22.6	362	2 JN0694	angiotensin II rec
32	405.5	22.3	359	2 I51372	angiotensin II rec
33	405	22.3	418	2 A46226	somatostatin recep
34	403	22.2	359	2 A48921	interleukin-8 rece
35	402	22.1	398	2 I56517	mu opioid receptor
36	402	22.1	428	2 I56517	probable G protein
37	401	22.1	356	2 S30508	interleukin-8 rece
38	401	22.1	356	2 S42096	interleukin-8 rece
39	401	22.1	358	2 A53752	interleukin-8 rece
40	399.5	22.0	398	2 A57510	mu opioid receptor
41	399.5	22.0	350	2 A39445	interleukin-8 rece
42	399.5	22.0	391	2 A41795	somatostatin recep
43	399.5	22.0	391	2 C41795	somatostatin recep
44	397	21.8	398	2 A39297	mu opioid receptor
45	396	21.8	392	2 S65693	opioid receptor mu

ALIGNMENTS

RESULT 1

B42009

FMLP-related receptor 1 - human

N:Alternate names: FMLP receptor homolog FPR2; formyl peptide receptor like-1; probab

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000

C:Accession: B42009; JCI1258; JQ1521; A42492; I54751; S21581

R:Ba0, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.

Genomics 13, 437-440, 1992

A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR

A:Reference number: A42009; MUID:92307681; PMID:1612600

A:Accession: B42009

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-263 'A', 265-338, 'C', 340-351 <BAO>

A:Cross-references: GB:M76672

A:Note: authors translated the codons GTG for residue 15 as Glu, TCT for residue 19 a

R:Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Andrews, W.H.

Gene 118, 303-304, 1992

A:Title: Cloning of a cDNA encoding a receptor related to the formyl peptide receptor

A:Reference number: JCI1258; MUID:92380523; PMID:1511907

A:Accession: JCI1258

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-351 <PER>

A:Cross-references: EMBL:X63819; NID:q31460; PID:g31461

A:Experimental source: bone marrow mRNA

R:Ye, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochran, C.G.

Biochem. Biophys. Res. Commun. 184, 582-589, 1992

A:Title: Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide recept

A:Reference number: JQ1521; MUID:92246937; PMID:1374236

A:Accession: JQ1521

A:Molecule type: mRNA

A:Residues: 1-351 <YE>

A:Cross-references: GB:M88107; NID:g189862; PID:g189863

A:Experimental source: granulocytes

A:Note: formyl peptide-stimulated calcium mobilization comparable to that of the form

R:Murphy, P.M.; Ozcelik, T.; Kenney, R.T.; Tiffany, H.L.; McDermott, D.; Francke, U.

J. Biol. Chem. 267, 7637-7643, 1992

A:Title: A structural homologue of the N-formyl peptide receptor. Characterization an

A:Reference number: A42492; MUID:92218423; PMID:1373134

A:Accession: A42492

A:Molecule type: mRNA

A:Residues: 1-351 <MUR>

A:Cross-references: GB:M84562; NID:g182741; PIDN:AAA52473.1; PID:g182742

A:Note: sequence extracted from NCBI backbone (NCBIN:94159, NCBIP:94160)

R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte c

A:Reference number: I54751; MUID:94092629; PMID:7505609

A:Accession: I54751

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-351 <RES>
A:Cross-references: GB:D10922; NID:g219864; PIDN:BA01720.1; PID:g219865
C:Comment: This G-protein coupled receptor, homologous to the N-formyl peptide receptor differentiated myeloid cells and is probably a chemotactic receptor for some other ligand
C:Genetics:
A:Gene: GDB:FPRL1
A:Cross-references: GDB:127554; OMIM:136538
A:Map position: 19q13.3-19q13.4
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein
F:27-53/Domain: transmembrane #status predicted <TM>
F:59-83/Domain: transmembrane #status predicted <TM>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:145-169/Domain: transmembrane #status predicted <TM4>
F:206-226/Domain: transmembrane #status predicted <TM5>
F:242-266/Domain: transmembrane #status predicted <TM6>
F:282-307/Domain: transmembrane #status predicted <TM7>
F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:98-176/Disulfide bonds: #status predicted
Query Match 100.0%; Score 1817; DB 2: Length 351;
Best Local Similarity 100.0%; Pred. No. 3.3e-145;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METNFTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVNGLVIVVAGFRMTRTVT 60
Db 1 METNFTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVNGLVIVVAGFRMTRTVT 60
QY 61 TICYLNALADSFATLPLFLIVSMAMGEKWPFGFGLCKLIHIVVDINLFGSVFLIGFTA 120
Db 61 TICYLNALADSFATLPLFLIVSMAMGEKWPFGFGLCKLIHIVVDINLFGSVFLIGFTA 120
QY 121 LDRICVLPVMAQNHRTVSLAMKVIVGPIIALVLTLPVFLFTVTTPNGDTCYTFNF 180
Db 121 LDRICVLPVMAQNHRTVSLAMKVIVGPIIALVLTLPVFLFTVTTPNGDTCYTFNF 180
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
Db 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
QY 241 RYLTAVASFFTCWPFQVALLGVTVLWKLKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300
Db 241 RYLTAVASFFTCWPFQVALLGVTVLWKLKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300
QY 301 LVYFVGQDPRERLIHSLPSSLERALS--DSAPTNDTAAASPPAETELQAM 351
Db 301 LVYFVGQDPRERLIHSLPSSLERALS--DSAPTNDTAAASPPAETELQAM 351
RESULT 2
FMLP-related receptor 2 - human
N:Alternate names: FMLP-related receptor 1; probable chemotactic receptor FPRH2
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C:Accession: C42009
R:Baou, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),
A:Reference number: A42009; MUID:92307681; PMID:1612600
A:Accession: C42009
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-353 <BAO>
A:Cross-references: GB:M76673; NID:g182668; PID:g182669
C:Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known, appears no
C:Genetics:
A:Gene: GDB:FPRL2
A:Cross-references: GDB:128855; OMIM:136539
A:Map position: 19q13.3-19q13.4
A:Introns: #status absent

C:Superfamily: vertebrate rhodopsin
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane prote
Query Match 72.5%; Score 1318; DB 2: Length 353;
Best Local Similarity 71.7%; Pred. No. 2.8e-103;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;
QY 1 METNFTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVNGLVIVVAGFRMTRTVT 60
Db 1 METNFTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVNGLVIVVAGFRMTRTVT 60
QY 61 TICYLNALADSFATLPLFLIVSMAMGEKWPFGFGLCKLIHIVVDINLFGSVFLIGFTA 120
Db 61 TICYLNALADSFATLPLFLIVSMAMGEKWPFGFGLCKLIHIVVDINLFGSVFLIGFTA 120
QY 121 LDRICVLPVMAQNHRTVSLAMKVIVGPIIALVLTLPVFLFTVTTPNGDTCYTFNF 180
Db 121 LDRICVLPVMAQNHRTVSLAMKVIVGPIIALVLTLPVFLFTVTTPNGDTCYTFNF 180
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
Db 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
QY 241 RYLTAVASFFTCWPFQVALLGVTVLWKLKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300
Db 241 RYLTAVASFFTCWPFQVALLGVTVLWKLKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300
QY 301 LVYFVGQDPRERLIHSLPSSLERALS--DSAPTNDTAAASPPAETELQAM 351
Db 301 LVYFVGQDPRERLIHSLPSSLERALS--DSAPTNDTAAASPPAETELQAM 351
RESULT 3
A42009
N-formyl peptide receptor - human
N:Alternate names: FMLP receptor
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
C:Accession: JC2014; A36309; A35495; A42009; I52414
R:Murphy, P.M.; Tiffany, H.L.; McDermott, D.; Ahuja, S.K.
Gene 133, 285-290, 1993
A:Title: Sequence and organization of the human N-formyl peptide receptor-encoding ge
A:Reference number: JC2014; MUID:94040825; PMID:8224916
A:Accession: JC2014
A:Molecule type: mRNA
A:Residues: 1-350 <MUR>
A:Cross-references: GB:L10820; NID:g182739; PIDN:AAAL6863.1; PID:g182740
R:Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P.
Biochemistry 29, 11123-11133, 1990
A:Title: The human N-formylpeptide receptor. Characterization of two cDNA isolates an
A:Reference number: A36309; MUID:91105045; PMID:2176894
A:Accession: A36309
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-191, 'N', 193-345, 'E', 347-350 <BOU1>
A:Cross-references: GB:M60627; GB:M33538; NID:g182664; PIDN:AAA35847.1; PID:g182665
R:Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P.
Biochem. Biophys. Res. Commun. 168, 1103-1109, 1990
A:Title: Synthesis and use of a novel N-formyl peptide derivative to isolate a human
A:Reference number: A35495; MUID:90267449; PMID:2161213
A:Accession: A35495
A:Molecule type: mRNA
A:Residues: 1-100, 'L', 102-191, 'N', 193-350 <BOU2>
A:Cross-references: GB:M37128; NID:g189183
A:Note: the sequence in GenBank entry HUNNFP, release 112.0, (PIDN:AAA36362.1) has t
R:Baou, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR)
A:Reference number: A42009; MUID:92307681; PMID:1612600
A:Accession: A42009
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1,'G',3-28,30-100,'L',102-104,106-112,'FLIA',115-176,178-182,184-191,'N',194
R;Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Chou, Q.; Andrews, W.H.
Biochemistry 31, 11595-11599, 1992
A:Title: Cloning of the gene coding for a human receptor for formyl peptides. Characteri
A:Reference number: I52414; MUID:93075765; PMID:1445895
A:Accession: I52414
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5 <PER>
A:Cross-references: GB:S49810; NID:g260832; PIDN:AAD14906.1; PID:g4262758
C:Genetics:
A:Gene: GDB:FPRI
A:Cross-references: GDB:127999; OMIM:136537
A:Map position: 19q13.4-19q13.4
A:Introns: #status absent
A:Note: entire coding region is found in exon 3; alternatively spliced mRNA transcripts
C:Superfamily: vertebrate rhodopsin
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein
F:53/Domain: transmembrane #status predicted <TM1>
F:59-83/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:145-169/Domain: transmembrane #status predicted <TM4>
F:206-225/Domain: transmembrane #status predicted <TM5>
F:242-266/Domain: transmembrane #status predicted <TM6>
F:279-304/Domain: transmembrane #status predicted <TM7>
F:4,10/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:98-176/disulfide bonds: #status predicted

Query Match 68.8%; Score 1249.5; DB 2; Length 350;
Best Local Similarity 68.9%; Pred. No. 1.6e-97;
Matches 241; Conservative 37; Mismatches 71; Indels 1; Gaps 1;

QY 1 METNFSPLNEEYEVESAGYTVLRILPLVLGVTVTVLGVGLNGLVIWAGFRMTT 60
DB 1 METNSSLPTNISGGTPAVSAGYFLDITLYLFAVTVLGVGLNGLVIWAGFRMTT 60
QY 61 TICVLNLALADFSFTATPLPLIVSMAMGEKWPFCWFLCKLIHIVVDNLFGSVFLIGFIA 120
DB 61 TISYLNALADFCFTSTLPFPFVIVTALGGHWPFGWFLCKFTFTIVDNLFGSVFLIALIA 120
QY 121 LDRICICVLHPVWQNRHTVSLAMKVIIVGVPWILALVLPVFLFTTTPNGDTYCTFNF 180
DB 121 LDRICVCLHPVWQNRHTVSLAMKVIIVGVPWILALVLPVFLFTTTPNGDTYCTFNF 180
QY 181 ASWGGTPEERLKVATMLTARGIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
DB 181 SPWTDNPKERIKAVAMLTVRGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
QY 241 RVLTAVVASFFICWFPFQVALLGTWVKEMLFYGYKIIDILVNPVTSLSAFAFNCLNPM 300
DB 241 RVLSFVAANFLCWSPPQVVALATVATVIRELL-QGMYKEIGIADVTSALAFNCLNPM 299
QY 301 LYFVVGQDFRERLIHSLPTSLERALSSEDSTNDTAANSAPPAETELQA 350
DB 300 LYFVVGQDFRERLIHALPASLERALTEDSTQTSATNTSLPSAEVALQA 349

RESULT 4
A46520
N-formyl peptide receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46520
R;Ye, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prossnitz, E.R.
J. Immunol. 150, 1383-1394, 1993
A:Title: The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression, and
A:Reference number: A46520; MUID:93163563; PMID:8432984
A:Accession: A46520
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-352 <YE1>
A:Cross-references: GB:M94549; NID:g165027; PIDN:AAA31254.1; PID:g165028
A:Experimental source: NZW, neutrophils

A:Note: sequence extracted from NCBI backbone (NCBIP:124908).
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match 67.3%; Score 1223.5; DB 2; Length 352;
Best Local Similarity 67.7%; Pred. No. 2.4e-95;
Matches 239; Conservative 41; Mismatches 70; Indels 3; Gaps 2;
QY 1 METNFSPLNEEYEVESAGYTVLRILPLVLGVTVTVLGVGLNGLVIWAGFRMTT 60
DB 1 MDSNASLPLNVSAGTQATPAGLVLDVFSYLILVTVTVLGVGLNGLVIWAGFRMTT 60
QY 61 TICVLNLALADFSFTATPLPLIVSMAMGEKWPFCWFLCKLIHIVVDNLFGSVFLIGFIA 120
DB 61 TISYLNALADFSFTSTLPFPFVIVTALGGHWPFGWFLCKFTFTIVDNLFGSVFLIALIA 120
QY 121 LDRICICVLHPVWQNRHTVSLAMKVIIVGVPWILALVLPVFLFTTTPN--GDTYCTF 178
DB 121 LDRICVCLHPVWQNRHTVSLAMKVIIVGVPWILALVLPVFLFTTTPN--GDTYCTF 180
QY 179 NFASWGGTPEERLKVATMLTARGIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSR 238
DB 181 DWSPTWEDPAEKLVKVAISMFMVVRGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSR 240
QY 239 PLRVLTAVVASFFICWFPFQVALLGTWVKEMLFYGYKIIDILVNPVTSLSAFAFNCLN 298
DB 241 PLRVLSFVWASFLCWSPPQVVALATVATVIRELL-GMGKDLRVLDVTSVAFNCLN 299
QY 299 PMLYFVGQDFRERLIHSLPTSLERALSSEDSTNDTAANSAPPAETELQAM 351
DB 300 PMLYFVGQDFRERLIHSLPASLERALSSEDSTQTSATNTSLPSAEVALQA 352

RESULT 5
A49542
N-formyl peptide chemotactic receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-Nov-1999
C:Accession: A49542
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 268, 25395-25401, 1993
A:Title: Species and subtype variants of the N-formyl peptide chemotactic receptor re
A:Reference number: A49542; MUID:94064602; PMID:8244972
A:Accession: A49542
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <GAO>
A:Cross-references: GB:L22181; NID:g347396; PIDN:AAA16110.1; PID:g347397
C:Genetics:
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: chemotaxis; transmembrane protein

Query Match 64.6%; Score 1174.5; DB 2; Length 364;
Best Local Similarity 64.6%; Pred. No. 3.3e-91;
Matches 237; Conservative 38; Mismatches 73; Indels 19; Gaps 5;
QY 1 METNFSPLNEEYEVESAGYTVLRILPLVLGVTVTVLGVGLNGLVIWAG 52
DB 1 MDTNMSLLMNKSAVNLNVSGTSQSVAGYIVLDVFSYLIFAVTVLGVGLNGLVIWAG 60
QY 53 FRMTRVTTCYLNALADFSFTATPLPLIVSMAMGEKWPFGWFLCKLIHIVVDNLFGS 112
DB 61 FRMKTHTTISYLNALADFCFTSTLPFPYITASVMYGGHWPFGWFLCKFTFTIVDNLFGS 120
QY 113 VFLIGFTALDRCICVLHPVWQNRHTVSLAMKVIIVGVPWILALVLPVFLFTTTPN- 171
DB 121 VFLIALDRCICVLHPVWQNRHTVSLAMKVIIVGVPWILALVLPVFLFTTTPN- 178
QY 172 ---GDTYCTFNFASWGGTPEERLKVATMLTARGIRFVIGFSLPMSIVAICYGLIAAK 227
DB 179 RLPGKTKACFDSPWTKDPVEKRVATMLTVRGIRFVIGFSLPMSIVAICYGLITTK 238

A;Residues: 1-350 <GER>
A;Cross-references: EMBL:X58674; NID:g295568; PIDN:CAB37830.1; PID:g4467832
R;Gerard, N.P.; Bao, L.; Xiao-Bing, H.; Eddy, R.L.
Biochemistry 32, 1243-1250, 1993
A;Title: Human chemotaxis receptor genes cluster at 19q13.3-13.4. Characterization of the
A;Reference number: 152417; MUID:93192225; PMID:8383526
A;Accession: 152417
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: cDNA
A;Residues: 1-3 <RES>
A;Cross-references: GB:S56556; GB:S56557; NID:g298577; NID:g298578
C;Genetics:
A;Gene: GDB:C5R1; C5A; C5AR
A;Cross-references: GDB:128956; OMIM:113995
A;Map position: 19q13.3-19q13.4
A;Introns: 1/3
A;Note: the list of introns may be incomplete
C;Function:
A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
n.
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorph
F;1-37/Domain: extracellular #status predicted <EX1>
F;38-61/Domain: transmembrane #status predicted <TM1>
F;62-71/Domain: intracellular #status predicted <IN1>
F;72-94/Domain: transmembrane #status predicted <TM2>
F;95-110/Domain: extracellular #status predicted <EX2>
F;111-132/Domain: transmembrane #status predicted <TM3>
F;133-149/Domain: intracellular #status predicted <IN2>
F;150-174/Domain: transmembrane #status predicted <TM4>
F;175-206/Domain: extracellular #status predicted <EX3>
F;207-227/Domain: transmembrane #status predicted <TM5>
F;228-242/Domain: intracellular #status predicted <IN3>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;265-283/Domain: extracellular #status predicted <EX4>
F;284-307/Domain: transmembrane #status predicted <TM7>
F;308-350/Domain: intracellular #status predicted <IN4>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.2%; Score 513; DB 1; Length 350;
Best Local Similarity 33.6%; Pred. No. 1.2e-35;
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

Qy 4 NFSIP-LNEYEE-----VSYESAGYTVLRILPLVVLGVTVTVLGVGLVGLNGLVWAGF 53
Db 5 NYTPDYGHYDDKDTLDLNTPTVDKTSNTLRVPDILALVIFAVFLVGLVGLNGLVWVWTF 64
Qy 54 RMTRVTTCYINLALADFSFTATLPFLIVSMAGEKWPFGWFLCKLIHIVVDINLFGSV 113
Db 65 EAKRTINAIWELNLAVALDFSLCALPILFTSIQVHHHPFGGAACSLILSLILNMYASI 124
Qy 114 FLIGFIALDRICIVLHPVWQAHNRVSLAMKVIVGPTILALVLPVFLFTVTIPNGD 173
Db 125 LLLATISADRELLVFKPIWCQNFGRAGLWACAVAGLALLLTPTSPFLRVV-----RE 179
Qy 174 TY-----CTNFASWGTPPEERLKVATMLTARGIIFVIGFSLPMSIVAICYLIAAK 227
Db 180 EYFPKVLGVGYSH-----DKRRRAV-----AIVRLVGLFLWPLTLTTCYTFILLR 228
Qy 228 IHKRGMIKSSRLRLVLTAVASFFFCPPFQVALLGVGLVGLNGLVWAGF 287
Db 229 TWSRRATSTKLVVAVASFFFLVLPYQVTGM-----MSFLEPSSFTLLNKL 281
Qy 288 SSL-----AFFNSCLNPMLYVFGQFRERLIHSLTSLERALSDESA-----PTND 334
Db 282 DSLCVSFAYINCCINPIIYVAGQFGQGRKRLKSLPSLLRNLTESVVRKSKFSTRSTD 341
Qy 335 TAA 337
Db 342 TMA 344

RESULT 9

S65766

G protein-coupled receptor (clone AZ3B) - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S65766
R;Roglic, A.; Prossnitz, E.R.; Cavanagh, S.L.; Pan, Z.; Zou, A.; Ye, R.D.
Biochim. Biophys. Acta 1305, 39-43, 1996
A;Title: cDNA cloning of a novel G protein-coupled receptor with a large extracellular
A;Reference number: S65766; MUID:96180983; PMID:8605247
A;Accession: S65766
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-482 <ROG>
A;Cross-references: EMBL:U28488; NID:g1199577; PIDN:AAC50374.1; PID:g1199578
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 28.0%; Score 509.5; DB 2; Length 482;
Best Local Similarity 26.6%; Pred. No. 3.4e-35;
Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

Qy 2 ETN-----FSTPLNEYEEVSYESAGYTVLRILPLVVLGVTVTVLGVGLNGLVWAGF 57
Db 7 ETNSTDLSSQWNEPPV-----ILSMVILSLTFLGLPGNGLVWVAVGLKMQR 54
Qy 58 TVTTCYINLALADFSFTATLPFLIVSMAGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117
Db 55 TVNTWFLHTLADLCLSLPFLSLAHLAGQWPGYGRFLCKLIPSIIVLNMFAVFLLT 114
Qy 118 FIALDRICIVLHPVWQAHNRVSLAMKVIVGPTILALVLPVFLFTVTIPNGDVTCT 177
Db 115 ALSDRCLVVPKPIWCQNHRRVGMACSGCIGIWWVAVFVVCIPVYVIREIFTTNDHNR-CG 173
Qy 178 FNFA-----
Db 174 YKFGLSLSLDYDFYGDPLENRSLENIQVPGEMNDRLDPSSFOFNDHPWVPTVFPQPT 233
Qy 184 -----GGTPEE-----R 190
Db 234 FQPSADSLPRGSARLTSONLYSNVFKPADVVPSPKIPSGFPFIEDHETSPLDSDAFLSTH 293
Qy 191 LKV-----AITMLTARGIIRFVIGFSLPMSIVA 218
Db 294 LKLPPSASSNFYSELPGQFDYINLQFTDDDDQVPLVAITITRLVVGFLLSVIMI 353
Qy 219 ICYGLIAAKIHKGMKIS-SRPLRVLTAVASFFFCPPFQVALLGVGLNGLVWAGF 277
Db 354 ACYSIFIVMRQGRFAKSKQSTFRVAVVAVFLVCWTPYHI-----F 396
Qy 278 KIIDLINPTS-----SLAFFNSCLNPMLYVFGQFRERLIHSLTSLER 323
Db 397 GVLSLTDPETPLGKTLMSWDHVCITALASANSFNPFLYALLGDKFRKARQSIQIGILEA 456
Qy 324 ALSDE-----SAPTNDDTAANSAS 341
Db 457 AFSEELTRSTHCPSPNNVISERN 479

RESULT 10

JC5796

probable chemoattractant receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: JC5796
R;Owman, C.; Lolait, S.J.; Santen, S.; Olde, B.
Biochem. Biophys. Res. Commun. 241, 390-394, 1997
A;Title: Molecular cloning and tissue distribution of a novel chemoattractant
A;Reference number: JC5796; MUID:98086361; PMID:9425281
A;Accession: JC5796
A;Molecule type: mRNA
A;Residues: 1-371 <OWM>
A;Cross-references: DDBJ:AJ002745; NID:g2624397; PIDN:CAA05715.1; PID:g2624398
A;Experimental source: liver

RESULT 15
JC2134
angiotensin II receptor type 1A - rat
N;Alternate names: AT1a receptor; AT3 receptor
C;Species: Rattus norvegicus (Norway rat)

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:15:57 ; Search time 14 Seconds
 (without alignments)
 1039.871 Million cell updates/sec

Title: US-09-944-807-2

Perfect score: 1817

Sequence: 1 METNFSPLNVEVSESA.....TNDTANSASPPAETELQAM 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1817	100.0	351	1 FMLL_HUMAN	P25090 homo sapien
2	1782	98.1	348	1 FMLL_PANTR	P79242 pan troglod
3	1781	98.0	348	1 FMLL_GORGO	P79177 gorilla gor
4	1744	96.0	348	1 FMLL_PONPY	P79236 pongo pygma
5	1740	95.8	348	1 FMLL_MACMU	P79190 macaca mula
6	1337	73.6	351	1 FMLL_MOUSE	O08790 mus musculu
7	1318	72.5	353	1 FMLL_HUMAN	P25089 homo sapien
8	1312	72.2	349	1 FMLL_PANTR	P79243 pan troglod
9	1304	71.8	349	1 FMLL_PONPY	P79237 pongo pygma
10	1299	71.5	349	1 FMLL_GORGO	P79178 gorilla gor
11	1292	71.1	349	1 FMLL_MACMU	P79191 macaca mula
12	1243.5	68.4	350	1 FMLR_HUMAN	P21462 homo sapien
13	1225.5	67.4	346	1 FMLR_PANTR	P79241 pan troglod
14	1225.5	67.4	346	1 FMLR_PONPY	P79235 pongo pygma
15	1223.5	67.3	352	1 FMLR_RABIT	Q05394 oryctolagus
16	1206.5	66.4	346	1 FMLR_GORGO	P79176 gorilla gor
17	1206.5	66.4	346	1 FMLR_MACMU	P79189 macaca mula
18	1174.5	64.6	364	1 FMLR_MOUSE	P33766 mus musculu
19	553.5	30.5	356	1 GP32_HUMAN	O75388 homo sapien
20	548.5	30.2	475	1 C3AR_CAVPO	O88680 cavia porce
21	542.5	29.9	477	1 C3AR_MOUSE	O09047 mus musculu
22	538.5	29.6	371	1 CMLL_MOUSE	P37468 mus musculu
23	534.5	29.4	373	1 CMLL_HUMAN	Q99788 homo sapien
24	530.5	29.2	382	1 GP44_MOUSE	Q92236 mus musculu
25	530.5	29.2	473	1 C3AR_RAT	O55197 rattus norv
26	513	28.2	350	1 C5AR_HUMAN	P21730 homo sapien
27	509.5	28.0	482	1 C3AR_HUMAN	O16581 homo sapien
28	508	28.0	340	1 C5AR_GORGO	P79175 gorilla gor
29	504.5	27.8	395	1 GP44_HUMAN	Q9y544 homo sapien
30	504	27.7	340	1 C5AR_PANTR	P79240 pan troglod
31	502.5	27.7	371	1 CMLL_RAT	O35786 rattus norv
32	502	27.6	353	1 GPRL_RAT	P46090 rattus norv
33	500	27.5	352	1 C5AR_CANFA	P30992 canis faml

34	499	27.5	340	1 C5AR_PONPY	P79234 pongo pygma
35	499	27.5	355	1 GPRL_HUMAN	P46091 homo sapien
36	499	27.5	355	1 GPRL_MACMU	O97664 macaca mula
37	489.5	26.9	350	1 C5AR_RABIT	Q9tuel oryctolagus
38	486	26.7	352	1 C5AR_RAT	P97520 rattus norv
39	483.5	26.6	340	1 C5AR_MACMU	P79188 macaca mula
40	472	26.0	340	1 GP33_MOUSE	O88416 mus musculu
41	458	25.2	347	1 C5AR_MOUSE	P30993 mus musculu
42	441	24.3	345	1 C5AR_CAVPO	O70129 cavia porce
43	434	23.9	356	1 IL8B_CANFA	O97571 canis faml
44	433	23.8	353	1 CCR4_FELCA	P56498 felis silve
45	430.5	23.7	359	1 AG2R_CAVPO	Q9wv26 cavia porce

ALIGNMENTS

RESULT 1					
FMLL_HUMAN					
ID	FMLL_HUMAN	STANDARD;	PRT;	351 AA.	
AC	P25090;				
DT	01-MAY-1992 (Rel. 22, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	FMLP-related receptor I (FMLP-R-1) (Lipoxin A4 receptor) (LXA4				
DE	receptor) (RFP) (HM63).				
GN	FPR1 OR FPR1 OR FPR2 OR LXA4R.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=92307681; PubMed=1612600;				
RA	Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;				
RT	"Mapping of genes for the human C5a receptor (C5AR), human FMLP				
RT	receptor (FPR), and two FMLP receptor homologue orphan receptors				
RT	(FPRH1, FPRH2) to chromosome 19.";				
RL	Genomics 13:437-440(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				
RA	MEDLINE=92380523; PubMed=1511907;				
RT	Perez H.D., Holmes R., Kelly E., McClary J., Andrews W.H.;				
RT	"Cloning of a cDNA encoding a receptor related to the formyl peptide				
RT	receptor of human neutrophils.";				
RL	Gene 118:303-304(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Granulocyte;				
RA	MEDLINE=92246937; PubMed=1374236;				
RA	Ye R.D., Cavanagh S.L., Quehenberger O., Prossnitz E.R.,				
RT	Cochrane C.G.;				
RT	"Isolation of a cDNA that encodes a novel granulocyte N-formyl				
RT	peptide receptor.";				
RL	Biochem. Biophys. Res. Commun. 184:582-589(1992).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=92218423; PubMed=1373134;				
RA	Murphy P.M., Ozcelik T., Kenney R.T., Tiffany H.L., McDermott D.,				
RA	Francie U.;				
RT	"A structural homologue of the N-formyl peptide receptor.				
RT	Characterization and chromosome mapping of a peptide chemoattractant				
RT	receptor family.";				
RL	J. Biol. Chem. 267:7637-7643(1992).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Monocytes;				
RA	MEDLINE=94092629; PubMed=7505609;				
RA	Nomura H., Nielsen B.W., Matsushima K.;				
RT	"Molecular cloning of cDNAs encoding a LD78 receptor and putative				
RT	leukocyte chemotactic peptide receptors.";				
RL	Int. Immunol. 5:1239-1249(1993).				

RN [6]
 RA SEQUENCE FROM N.A.
 RP Maddox J.F., Hachicha M., Takano T., Petasis N.A., Fokin V.V.,
 RA Serhan C.N.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RA SEQUENCE FROM N.A.
 RP MEDLINE=98215774; PubMed=9547339;
 RX Grontz K., Gewirtz A., Madara J.L., Serhan C.N.;
 RA "Identification of a human enterocyte lipoxin A4 receptor that is
 RT regulated by interleukin (IL)-13 and interferon gamma and inhibits
 RT tumor necrosis factor alpha-induced IL-8 release";
 RL J. Exp. Med. 187:1285-1294 (1998).
 RN [8]
 RA SEQUENCE FROM N.A.
 RP Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise I., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RA TISSUE SPECIFICITY.
 RP MEDLINE=97296322; PubMed=9151906;
 RX Takano T., Fiore S., Maddox J.F., Brady H.R., Petasis N.A.,
 RA Serhan C.N.;
 RA "Aspirin-triggered 15-epi-lipoxin A4 (LXA4) and LXA4 stable analogues
 RT are potent inhibitors of acute inflammation: evidence for
 RT anti-inflammatory receptors";
 RL J. Exp. Med. 185:1693-1704 (1997).
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
 CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
 CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THE
 CC ACTIVATION OF LXA4R COULD RESULT IN AN ANTI-INFLAMMATORY OUTCOME
 CC COUNTERACTING THE ACTIONS OF PROINFLAMMATORY SIGNALS SUCH AS LTB4
 CC (LEUKOTRIENE B4).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN THE LUNG AND
 CC NEUTROPHILS. ALSO FOUND IN THE SPLEEN AND TESTIS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL; M76672; AAA58481.1; -;
 DR EMBL; X63819; CAA45319.1; -;
 DR EMBL; M88107; AAA60070.1; -;
 DR EMBL; M84562; AAA52473.1; -;
 DR EMBL; U10922; BAA01720.1; -;
 DR EMBL; U81501; AAB51133.1; -;
 DR EMBL; AF054013; AAC13684.1; -;
 DR EMBL; AC018755; AAF87844.1; -;
 DR PIR; JC1258; JC1258.
 DR PIR; A42492; A42492.
 DR PIR; JQ1521; JQ1521.
 DR PIR; B42009; B42009.
 DR HSSP; P34996; 1DDD.
 DR Genew; HGNC:3827; FPRLL1.
 DR MIM; 136538; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 28 50 1 (POTENTIAL).
 FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 62 83 2 (POTENTIAL).
 FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 121 3 (POTENTIAL).
 FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 141 162 4 (POTENTIAL).
 FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226 5 (POTENTIAL).
 FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 266 6 (POTENTIAL).
 FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 306 7 (POTENTIAL).
 FT DOMAIN 307 351 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 98 176 POTENTIAL.
 FT CONFLICT 339 S -> C (IN REF. 1).
 SQ SEQUENCE 351 AA: 38964 MW: DC6A1D77AFC0D780 CRC64;
 Query Match 100.0%; Score 1817; DB 1; Length 351;
 Best Local Similarity 100.0%; Pred. No. 1e-97;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METNESTPLNEEYEEVSAGYTVLRILPVVLGVTVFVLGNGLVIVWAGFRMTRTVT 60
 DB 1 METNESTPLNEEYEEVSAGYTVLRILPVVLGVTVFVLGNGLVIVWAGFRMTRTVT 60
 QY 61 TICYLNALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHVVDINLFGSVFLIGFTA 120
 DB 61 TICYLNALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHVVDINLFGSVFLIGFTA 120
 QY 121 LDRICVLPVWQAQNHRTVSLAMKVIWGPWILALVTLTPVFLFVLTVPNGDTCYTFNF 180
 DB 121 LDRICVLPVWQAQNHRTVSLAMKVIWGPWILALVTLTPVFLFVLTVPNGDTCYTFNF 180
 QY 181 ASWGTPPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
 DB 181 ASWGTPPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
 QY 241 RVLTVAVASFFCWPFQVALLGVTVLWVKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300
 DB 241 RVLTVAVASFFCWPFQVALLGVTVLWVKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSSEDSAPTNDTAANSASPPAETELQAM 351
 DB 301 LVYFVGQDFRERLIHSLPTSLERALSSEDSAPTNDTAANSASPPAETELQAM 351

RESULT 2

FML1_PANTR
 ID FML1_PANTR STANDARD; PRT; 348 AA.
 AC P79242;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE FMLP-related receptor I (FMLP-R-I) (Fragment).
 GN FPRLL.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96421539; PubMed=8824156;
 RA Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in
 RL non-human primates";
 RL Immunogenetics 44:446-452 (1996).
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,

CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; X97739; CAA66323.1; -;
CC HSP; P34996; IDDD.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC NON_TER 1 1
CC DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 25 47 1 (POTENTIAL).
CC DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 59 80 2 (POTENTIAL).
CC DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 98 118 3 (POTENTIAL).
CC DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 138 159 4 (POTENTIAL).
CC DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 203 223 5 (POTENTIAL).
CC DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 240 263 6 (POTENTIAL).
CC DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 284 303 7 (POTENTIAL).
CC DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 1 1 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 95 173 POTENTIAL.
CC NON_TER 348 348
CC SEQUENCE 348 AA; 38574 MW; 55B76670DF4D594E CRC64;
Query Match 98.1%; Score 1782; DB 1; Length 348;
Best Local Similarity 98.9%; Pred. No. le-95;
Matches 344; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 4 NFSTPLNEYEVESAGYTVLRILPLVGLVGVTFVLGVLGNGLVWVAGFRMTRITVTTIC 63
Db 1 NFSTPLNEYEVESAGYTVLRILPLVGLVGVTFVLGVLGNGLVWVAGFRMTRITVTTIC 60
Qy 64 YLNALADFSFTATLPFLIVSMANGKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDR 123
Db 61 YLNALADFSFTATLPFLIVSMANGKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDR 120
Qy 124 CICVLHPWAQNHRTVSLAMKVIIVGPWILALVLPFLFTTTPINGDYCTCFNFASW 183
Db 121 CICVLHPWAQNHRTVSLAMKVIIVGPWILALVLPFLFTTTPINGDYCTCFNFASW 180
Qy 184 GGTPEERLKVAITLMTARGIIRFVIGFSLPMSIVAICVGLIAAKTHKKGMKSSRPLRLV 243
Db 181 GGTPEERLKVAITLMTARGIIRFVIGFSLPMSIVAICVGLIAAKTHKKGMKSSRPLRLV 240
Qy 244 TAVVASFFICWFPFQVALLGTVMKEMLFYKGYKIIIDILVNPSTSSLAFFNCLNPMILV 303
Db 241 TAVVASFFICWFPFQVALLGTVMKEMLFYKGYKIIIDILVNPSTSSLAFFNCLNPMILV 300
Qy 304 FVGQDFRRLHLSPTSLERALSSEDAPTNDTAANSAPPAETELQAM 351
Db 301 FVGQDFRRLHLSPTSLERALSSEDAPTNDTAANSAPPAETELQAM 348

RESULT 3
FMLL_GORGO STANDARD; PRT; 348 AA.
AC P79177;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMLP-related receptor I (FMLP-R-I) (Fragment).
GN FPLLI.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=8824156;
RA Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in
RT non-human primates.";
RL Immunogenetics 44:446-452(1996).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; X97738; CAA66322.1; -;
CC HSP; P34996; IDDD.
CC InterPro; IPR000276; GPCR_Rhodpsn.
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CC PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
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CC DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 25 47 1 (POTENTIAL).
CC DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 59 80 2 (POTENTIAL).
CC DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 98 118 3 (POTENTIAL).
CC DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 138 159 4 (POTENTIAL).
CC DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 203 223 5 (POTENTIAL).
CC DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 240 263 6 (POTENTIAL).
CC DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 284 303 7 (POTENTIAL).
CC DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 1 1 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 95 173 POTENTIAL.
CC NON_TER 348 348
CC SEQUENCE 348 AA; 38580 MW; B1F0B3BDCC76CAA0 CRC64;
Query Match 98.0%; Score 1781; DB 1; Length 348;
Best Local Similarity 98.9%; Pred. No. 1.2e-95;
Matches 344; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 4 NFSTPLNEYEVESAGYTVLRILPLVGLVGVTFVLGVLGNGLVWVAGFRMTRITVTTIC 63
Db 1 NFSTPLNEYEVESAGYTVLRILPLVGLVGVTFVLGVLGNGLVWVAGFRMTRITVTTIC 60

QY 64 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHVVVDINLFGSVFLIGFIALDR 123
 DB 61 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHVVVDINLFGSVFLIGFIALDR 120
 QY 124 CICVLHPVWQAQNHRTVSLAMKVIIGPWLALVLTLPVFLFTVTPNGDTCYCFENFASW 183
 DB 121 CICVLHPVWQAQNHRTVSLAMKVIIGPWLALVLTLPVFLFTVTPNGDTCYCFENFASW 180
 QY 184 GGTPEERLKVATMTLTARIIIFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 243
 DB 181 GGTPEERLKVATMTLTARIIIFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 240
 QY 244 TAVASFFICWPFQVALLGVWLVKEMLFYGYKIIDILVNPTSSLAFFNSCLNPMYLV 303
 DB 241 TAVASFFICWPFQVALLGVWLVKEMLFYGYKIIDILVNPTSSLAFFNSCLNPMYLV 300
 QY 304 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 351
 DB 301 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 348

RESULT 4

FT DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 203 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 263 6 (POTENTIAL).
 FT DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 284 303 7 (POTENTIAL).
 FT DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 1 1 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 95 173 POTENTIAL.
 FT NON_TER 348 348
 SQ SEQUENCE 348 AA; 38686 MW; ES44D005CFA41616 CRC64;
 Query Match 96.0%; Score 1744; DB 1; Length 348;
 Best Local Similarity 96.6%; Pred. No. 1.5e-93;
 Matches 336; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 4 NFSTPLNEEVSYESAGTYVLRILPLVVLGVTFVLGVGLNGLVWVAGFRMTRVTTC 63
 DB 1 NFSTPLNEEVSYESAGTYVLRILPLVVLGVTFVLGVGLNGLVWVAGFRMTRVTTC 60
 QY 64 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHVVVDINLFGSVFLIGFIALDR 123
 DB 61 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHVVVDINLFGSVFLIGFIALDR 120
 QY 124 CICVLHPVWQAQNHRTVSLAMKVIIGPWLALVLTLPVFLFTVTPNGDTCYCFENFASW 183
 DB 121 CICVLHPVWQAQNHRTVSLAMKVIIGPWLALVLTLPVFLFTVTPNGDTCYCFENFASW 180
 QY 184 GGTPEERLKVATMTLTARIIIFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 243
 DB 181 GGTPEERLKVATMTLTARIIIFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 240
 QY 244 TAVASFFICWPFQVALLGVWLVKEMLFYGYKIIDILVNPTSSLAFFNSCLNPMYLV 303
 DB 241 TAVASFFICWPFQVALLGVWLVKEMLFYGYKIIDILVNPTSSLAFFNSCLNPMYLV 300
 QY 304 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 351
 DB 301 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 348

RESULT 5
 ID FMLI_MACMU STANDARD; PRT; 348 AA.
 AC P79190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE FMLP-related receptor I (FMLP-R-1) (fragment).
 GN FPR1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RX SEQUENCE FROM N.A.
 RX MEDLINE=96421539; PubMed=8824156;
 RA Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-human primates";
 RL Immunogenetics 44:446-452(1996).
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL; X97744; CAA6328.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; transmembrane; Glycoprotein;
 KW ChemoTaxis.
 FT NON_TER 1 1
 FT DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 25 47 1 (POTENTIAL).
 FT DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 80 2 (POTENTIAL).
 FT DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 98 118 3 (POTENTIAL).
 FT DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 138 159 4 (POTENTIAL).


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Db 61 TWYLNALADSFATLFLVLVEMAKKWPFGFLCKLVHADVNLFGSVFLIAVIA 120
QY 121 LDRICVLPVWQAQNRHTVSLAMKVIQVGPWILALVLTLPVFLFLTTVTPNGDTCYTFNF 180
Db 121 LDRICVLPVWQAQNRHTVSLARNVVGWIFALILTLPLEFLTLTVRDARGDVHCLRSF 180
QY 181 ASWGGTPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMKIKSRRLP 240
Db 181 VSGNSVEERLNTATITFVTRGIRFIVFSFSLPMSFVAICYGLITTKHKKAFVNSRRP 240
QY 241 RYLTAVASFFTCWPFQVALLGVWVKEMLFYKIKIIDLIVNPTSSLAFFNSCLNPM 300
Db 241 RYLTGVASFFTCWPFQVALLGVWVKEMQFSGYKIGRLVNPSSLAFFNSCLNPI 300
QY 301 LYVFGQDFRERLIHSLPTSLERLSEDSAPTNDTAANSASPPAETELQAM 351
Db 301 LYVFMGQDFRERLIHSLPTSLERLSEDSGHSIDRTNLSLPEDIEIKAI 351

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RESULT 7

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ID FML2_HUMAN STANDARD; PRT; 353 AA.
AC P25089;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE FMLP-related receptor II (FMLP-R-II).
GN FPLR2 OR FPRH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307681; PubMed=1612600;
RA Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;
RT "Mapping of genes for the human C5a receptor (C5AR), human FMLP
RT receptor (FPR), and two FMLP receptor homologue orphan receptors
RT (FPRH1, FPRH2) to chromosome 19."
RL Genomics 13:437-440(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256976; PubMed=8198572;
RA Durstin M., Gao J.-L., Tiffany H.L., McDermott D., Murphy P.M.;
RT "Differential expression of members of the N-formylpeptide receptor
RT gene cluster in human phagocytes."
RL Biochem. Biophys. Res. Commun. 201:174-179(1994).
CC -!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; M76573; AAA58482.1; -.
CC EMBL; L14061; AAA52474.1; -.
CC PIR; C42009; C42009
CC Genew; HGNC:3826; FPLR2.
CC MIM; 136539; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.

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DR PROSITE; PS00262; G_PROTEIN_RECEP_FL1; 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 51 1 (POTENTIAL).
FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 83 2 (POTENTIAL).
FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 162 4 (POTENTIAL).
FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 266 6 (POTENTIAL).
FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 306 7 (POTENTIAL).
FT DOMAIN 307 353 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 98 176 POTENTIAL.
FT CONFLICT 94 94 A -> G (IN REF. 2).
FT CONFLICT 211 211 T -> S (IN REF. 2).
FT CONFLICT 338 338 H -> D (IN REF. 2).
SQ SEQUENCE 353 AA; 40015 MW; 8ED7450A14A36C9A CRC64;

Query Match 72.5%; Score 1318; DB 1; Length 353;
Best Local Similarity 71.7%; Pred. No. 3.7e-69;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

QY 1 METNFTPLNEEVEEVSAGYTVLRILPLVVLGVTVFVLGVGLNGLVIVWAGFRMTRVT 60
DB 1 METNFSIPLNEEVLPEPAGHTLWIFSLVHGVTFVGVGLNGLVIVWAGFRMTRVN 60
QY 61 TICYNLALADSFATLFLVLVEMAKKWPFGFLCKLVHADVNLFGSVFLIGFTA 120
DB 61 TICYNLALADSFATLFLVFRVSVAMREKWPFGFASFLCKLVHMDINLFSVYLITIA 120
QY 121 LDRICVLPVWQAQNRHTVSLAMKVIQVGPWILALVLTLPVFLFLTTVTPNGDTCYTFNF 180
DB 121 LDRICVLPVWQAQNRHTVSLAKRVMTGLMIFTIVLTPNFIFWTITSTNGDTCYCFNF 180
QY 181 ASWGGTPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMKIKSRRLP 240
DB 181 AFWGDTAVERLNVFTIMAKVFLIHFIIGFTVPMSTIITVCYGLIAAKIHRNMHKSRRLP 240
QY 241 RYLTAVASFFTCWPFQVALLGVWVKEMLFYKIKIIDLIVNPTSSLAFFNSCLNPM 300
DB 241 RVFAAVASFFTCWPFYELIGILMAVWLKEMLLNGYKILVLIINPTSSLAFFNSCLNPI 300
QY 301 LYVFGQDFRERLIHSLPTSLERLSE--DSAPTNDTAANSASPPAETELQAM 351
DB 301 LYVFMGRNFRERLIHSLPTSLERALTVEPDSAQTSNTHTTSASPPETELQAM 353

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RESULT 8

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ID FML2_PANTR STANDARD; PRT; 349 AA.
AC P79243;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE N-formyl peptide receptor-like 2 receptor (Fragment).
GN FPRL2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_Taxid=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=8824156;
RA Alvarez V., Coto E., Sehén F., Gouzalet-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in

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RT non-human primates *;
CC Immunogenetics 44:446-452(1996).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC FMPL TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL: X97743; CAA66327.1; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PROSITE: PS00237; G-PROTEIN_RECF1_1; 1.
CC PROSITE: PS0262; G-PROTEIN_RECF1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 28 50 1 (POTENTIAL).
CC DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 62 83 2 (POTENTIAL).
CC DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 101 121 3 (POTENTIAL).
CC DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 141 162 4 (POTENTIAL).
CC DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 206 226 5 (POTENTIAL).
CC DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 243 266 6 (POTENTIAL).
CC DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 287 306 7 (POTENTIAL).
CC DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
CC DISULFID 98 176 POTENTIAL.
CC NON_TER 349 349
CC SEQUENCE 349 AA; 88279F8C72915383 CRC64;

Query Match 72.28; Score 1312; DB 1; Length 349;
Best Local Similarity 72.28; Pred. No. 8e-69;
Matches 252; Conservative 37; Mismatches 58; Indels 2; Gaps 1;

Qy 1 METNFTPLNEYEVESYAGYTVLRILPLVLGVVTVFVGLVGLNGLVWVAGFRMTRVT 60
Db 1 METNFSIPLNETEEVLPFAGHTVLIWIFSLVHGVTFFVGLVGLNGLVWVAGFRMTRVN 60
Qy 61 TICVNLALADFSFATLPELIVSMGCEKWPFGNFKLKHIVVDINLEGSVFLIGFTA 120
Db 61 TICVNLALADFSFATLPELIVSMGCEKWPFGNFKLKHIVVDINLEGSVFLIGFTA 120
Qy 121 LDRICVILHPVWQNHRTVSAMKVIYGVFWILALVLTLPVFLFTLTVPNGDITYCTENF 180
Db 121 LDRICVILHPVWQNHRTVSAMKVIYGVFWILALVLTLPVFLFTLTVPNGDITYCTENF 180
Qy 181 ASWGGTPPEERKVAITMTARGITRFVGFSLPMSIVAICYGLIAAKTHKKGMKSSRPL 240
Db 181 ASWGGTPPEERKVAITMTARGITRFVGFSLPMSIVAICYGLIAAKTHKKGMKSSRPL 240
Qy 181 AFWGDTAVERNVFTAKVFLILHFIIGFSNPMWSIIIVCYGIIAAKTHRNHMKSSRPL 240
Db 181 AFWGDTAVERNVFTAKVFLILHFIIGFSNPMWSIIIVCYGIIAAKTHRNHMKSSRPL 240
Qy 241 RVLTAVASFTICFPFOLVALLGKEMLFYCKYKIIIDLVNPTSSLAFFNSCLNPM 300
Db 241 RVLTAVASFTICFPFOLVALLGKEMLFYCKYKIIIDLVNPTSSLAFFNSCLNPM 300
Qy 301 LYVFGQDFRERLHSLPTSLERALSE--DSAPTNDTAANSAPPAETE 347
Db 301 LYVFGQDFRERLHSLPTSLERALSE--DSAPTNDTAANSAPPAETE 347
Qy 301 LYVFGNFRQERLRSPTSLERALTVEPDSAQTSNTHHTSAPPEETE 349
Db 301 LYVFGNFRQERLRSPTSLERALTVEPDSAQTSNTHHTSAPPEETE 349

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RESULT 9
FML2_PONPY STANDARD; PRT; 349 AA.
ID FML2_PONPY
AC P79237;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE N-formyl peptide receptor-like 2 receptor (Fragment).
GN FPRL2.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=88241156;
RT Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in
RT non-human primates.";
RL Immunogenetics 44:446-452(1996).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC FMPL TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X97741; CAA66325.1; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PROSITE: PS00237; G-PROTEIN_RECF1_1; 1.
CC PROSITE: PS0262; G-PROTEIN_RECF1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 28 50 1 (POTENTIAL).
CC DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 62 83 2 (POTENTIAL).
CC DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 101 121 3 (POTENTIAL).
CC DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 141 162 4 (POTENTIAL).
CC DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 206 226 5 (POTENTIAL).
CC DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 243 266 6 (POTENTIAL).
CC DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 287 306 7 (POTENTIAL).
CC DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
CC DISULFID 98 176 POTENTIAL.
CC NON_TER 349 349
CC SEQUENCE 349 AA; 39423 MW; C8298D223395EBC CRC64;

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Query Match 71.8%; Score 1304; DB 1; Length 349;
Best Local Similarity 71.6%; Pred. No. 2.3e-68;
Matches 250; Conservative 39; Mismatches 58; Indels 2; Gaps 1;

Qy 1 METNFTPLNEYEVESYAGYTVLRILPLVLGVVTVFVGLVGLNGLVWVAGFRMTRVT 60
Db 1 METNFSIPLNETEEVLPFAGHTVLIWIFSLVHGVTFFVGLVGLNGLVWVAGFRMTRVN 60

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FT	DOMAIN	163	205	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	206	226	5 (POTENTIAL).
FT	DOMAIN	227	242	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	243	266	6 (POTENTIAL).
FT	DOMAIN	267	286	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	287	306	7 (POTENTIAL).
FT	DOMAIN	307	>349	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	4	4	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	10	10	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	98	176	POTENTIAL.
FT	NON_TER	349	349	
SO	SEQUENCE	349 AA;	39432 MW;	C6ED77CFDE023834 CRC64;

Query Match	71.5%;	Score 1299;	DB 1;	Length 349;
Best Local Similarity	71.3%;	Pred. NO. 4.4e-68;		
Matches 249;	Conservative 38;	Mismatches 60;	Indels 2;	Gaps

QY	1	MEYFNSTPLN	EEVSEYAGYTVLRILPLVVLGVGTVFLVGLGNGLVIVWAGFMRTRVT	60
DB	1	MEYFNSTPLN	TEEVLPEPAGHTVLMFSLVLLVHGVTIFGVGLGNGLVIVWAGFLMTRTVN	60
QY	61	TICYLNIALAD	FSFTATPLPLIVSMAMGEKWPGEWFLCKLIHIVVDINLVGSVFLIGFIA	120
DB	61	TICYLNIALAD	FSFSAILLPHMYSVAMREKWPGEFLCKLVHVMIDINLVSVYLITIIA	120
QY	121	LDRICICVLHP	VWAGNHTVSLAMKVLVGPWILALVLTLPVFLFTVTPNGDGYCTCFNF	180
DB	121	LDRICICVLHP	WAGNHTVSLAKRVMTGWLIVTLVLPNFIPWTTISTNGDYTCIFNF	180
QY	181	ASGGGTPEER	LKVAITMLTARGIIRFVIGFSLPMSVAICYGLIAAKIHKKGMKSSRPL	240
DB	181	PPWGDRAVER	LNVFITMAKVFLLHFIIGFSMPMSIITVCYGIIAAKIHKNHMKSSRPL	240
QY	241	RVLTAVVASP	FCWPFQFVALLGTVLWKEMLEPYGKYKIIDIILVNPTSSLAFFNSCLNPM	300
DB	241	RVFAAVVASP	FCWPFYELIGILMAYMLKEMLINGKYKIILVINPTSSLAFFNSCLNI	300
QY	301	LYVFGVDGFR	ELIHSIPTSLSRALSE--DSAPNTDAANSAPPAETE	347
DB	301	LYVFLGNSQER	LIRSLIPTSLSRALTEVPDSQTSNHTHTSAPPEETE	349

RESULT 11	FML2_MACMU	STANDARD;	PRT;	349 AA.
ID	FML2_MACMU			
AC	P79191;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DE	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	N-formyl peptide receptor-like 2 receptor (Fragment).			
GN	FPRL2.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_Taxid=9544;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=96421539; PubMed=8824156;			
RA	Alvarez V., Coto E., Selen F., Gouzalak-Koces S., Lopez-Larrea C.;			
RT	"Molecular evolution of the N-formyl peptide and C5a receptors in			
RT	non-human primates."			
RL	Immunogenetics 44:446-452(1996).			
CC	-1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,			
CC	WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF			
CC	FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS			
CC	RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A			
CC	PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstar			

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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: X97740; CAA66324.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 28 50 1 (POTENTIAL).
 FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 62 83 2 (POTENTIAL).
 FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 121 3 (POTENTIAL).
 FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 141 162 4 (POTENTIAL).
 FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226 5 (POTENTIAL).
 FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 266 6 (POTENTIAL).
 FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 306 7 (POTENTIAL).
 FT DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 98 176 POTENTIAL.
 FT NON_TER 349 349
 SQ SEQUENCE 349 AA; 39531 MW; C0C92A9B5CDE2250C CRC64;

Query Match 71.1%; Score 1292; DB 1; Length 349;
 Best Local Similarity 70.5%; Pred. No. 1.1e-67;
 Matches 246; Conservative 39; Mismatches 62; Indels 2; Gaps 1;

QY 1 METNFSPLNNEYEVSYESAGYTVLRILPLVLGVTVFVLGVNGLVWVAGFRMTRVT 60
 Db 1 METNFSPLNNEYEVSYESAGYTVLRILPLVLGVTVFVLGVNGLVWVAGFRMTRVT 60
 QY 61 TICVNLALADFSATLPLFLIVSMANGKWPFGWFKLHIVVDNLFGSVPLIGFIA 120
 Db 61 TICVNLALADFSATLPLFLIVSMANGKWPFGWFKLHIVVDNLFGSVPLIGFIA 120
 QY 121 LDRICVLPVWQAQNHRTVSLAMKVIVGVPTLALVLPVPLFTTTPNGDYCTCFNF 180
 Db 121 LDRICVLPVWQAQNHRTVSLAMKVIVGVPTLALVLPVPLFTTTPNGDYCTCFNF 180
 QY 181 ASWGGTPEERLKVATMLTARGITRVFVIGSLPMSVAICVGLIAAKIHKMGTKSSRPL 240
 Db 181 ASWGGTPEERLKVATMLTARGITRVFVIGSLPMSVAICVGLIAAKIHKMGTKSSRPL 240
 QY 241 RVLTAVASFFICWFPQVALLGTVLWVEMLVYKVKIIDLVPNTSSLAFFNSCLNPM 300
 Db 241 RVLTAVASFFICWFPQVALLGTVLWVEMLVYKVKIIDLVPNTSSLAFFNSCLNPM 300
 QY 301 LYFVVGQDFRRLRHLISLPTSLERALSE--DSAPNTNDTAANSASPAETE 347
 Db 301 LYFVVGQDFRRLRHLISLPTSLERALSE--DSAPNTNDTAANSASPAETE 347

RESULT 12

FMLR_HUMAN

ID FMLR_HUMAN STANDARD; PRT; 350 AA.

AC P21462; O14939; Q9NS48;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE fMet-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)

DE (fPR) (N-formyl peptide chemoattractant receptor).

GN FPRL.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90267449; PubMed=2161213;
 RA Boulay F., Tardif M., Bouchon L., Vignais P.;
 RT "Synthesis and use of a novel N-formyl peptide derivative to isolate
 RL a human N-formyl peptide receptor cDNA.";
 RN Biochem. Biophys. Res. Commun. 168:1103-1109(1990).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91105045; PubMed=2176894;
 RA Boulay F., Tardif M., Bouchon L., Vignais P.;
 RT "The human N-formylpeptide receptor. Characterization of two cDNA
 RL isolates and evidence for a new subfamily of G-protein-coupled
 RN receptors.";
 RN Biochemistry 29:11123-11133(1990).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91286286; PubMed=1712023;
 RA Murphy P.M., McDermott D.;
 RT "Functional expression of the human formyl peptide receptor in
 RL Xenopus oocytes requires a complementary human factor.";
 RN J. Biol. Chem. 266:12560-12567(1991).
 [4]
 RP SEQUENCE FROM N.A.
 RA Perez H.D.;
 RL Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94040825; PubMed=8224916;
 RA Murphy P.M., Tiffany H.L., McDermott D., Ahuja S.K.;
 RT "Sequence and organization of the human N-formyl peptide receptor-
 RL encoding gene.";
 RN Gene 133:285-290(1993).
 [6]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McGready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of a 5-Mb region in 19q13.4.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,
 CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
 CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: NEUTROPHILS.
 CC -1- POLYMORPHISM: THE VARIANT SEQUENCES ARE THOUGHT TO BE DUE TO
 CC ALLELIC VARIATION OF A SINGLE GENE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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DR EMBL; M37128; AAA36362.1; -
DR EMBL; M60626; AAA35846.1; -
DR EMBL; M60627; AAA35847.1; -
DR EMBL; L10820; AAA16863.1; -
DR EMBL; AC018755; AAF87842.1; -
DR EMBL; BC005315; AAH05315.1; -
DR PIR; A35495; A35495
DR PIR; A36309; A36309
DR Genew; HGNC:3826; FPR1.
DR MIM; 136537; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis; Polymorphism.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 50 1 (POTENTIAL).
FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 83 2 (POTENTIAL).
FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 162 4 (POTENTIAL).
FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 266 6 (POTENTIAL).
FT DOMAIN 267 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 305 7 (POTENTIAL).
FT DOMAIN 306 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 98 176 POTENTIAL.
FT VARIANT 101 101 L -> V.
FT VARIANT 192 192 /FTid=VAR_003476.
FT VARIANT 192 192 N -> K.
FT VARIANT 346 346 /FTid=VAR_003477.
FT VARIANT 346 346 A -> E.
FT CONFLICT 238 238 /FTid=VAR_003478.
FT CONFLICT 238 238 R -> P (IN REF. 1).
SQ SEQUENCE 350 AA; 38401 MW; 0663EFF8267E2BD1 CRC64;
Query Match 68.4%; Score 1243.5; DB 1; Length 350;
Best Local Similarity 68.6%; Pred. No. 6.6e-65;
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;
1 METNSTPLNEYEVESAGYTVLRILPLVGLVTVGLVGLNGLVWVAGFRMTRVT 60
1 METNSLPNISGGTPAVSAGYLFIDITVLFVAVTVGLVGLNGLVWVAGFRMTRVT 60
61 TICYNLALADFSFATLPLFLIVSMAMGEKWPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120
61 TISYLNLAADVPCFTSTLPFFVMVRKAMGHPFGWFLCKLFTIIVDINLFGSVFLIALIA 120
121 LDRICVLPVWQNRHVSAMKVIIVGFWILALVLTLPVLEFVTVTPNGDVTCTENF 180
121 LDRICVLPVWQNRHVSAMKVIIVGFWILALVLTLPVLEFVTVTPNGDVTCTENF 180
181 ASWGCTPPEERLKVATITMTARGIIRFVGLSPMSIVAIQVIAKTHKKMKSSRPL 240
181 SPWVNDPKRINVAAMTVIRGIRFIIFGAPMSIVAVSGLIATKIKHKGILKSSRPL 240
241 RYLTAVASFFICWPFQVALLGFWLWVLEKEMLFYKGIKIIDILVNPTSSLAFFNSCLNPM 300
241 RYLSVPAFAFFLWSPYQVVALIATVIRELL-QGMYKEIGIADVDTVSALAFFNSCLNPM 299
301 LYVFGQDFRERLIHSLTSLERALSDESAPTNDAANSAPPAETELOA 350
300 LYVFMGQDFRERLIHALPASLERALTEDSTQTSATNTSLFSAEVALQA 349

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RESULT 13
FMLR_PANTR STANDARD; PRT; 346 AA.
AC DT 15-JUL-1998 (Rel. 36, Created)
AC P79241;
AT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE fMet-leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)
DE (FPR) (N-formylpeptide chemoattractant receptor) (Fragment).
GN FPR1.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=8824156;
RA Alvarez V., Coto E., Sehen F., Gouzaiek-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in
RL non-human primates.";
RL Immunogenetics 44:446-452(1996).
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X97745; CAA66329.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT NON_TER 1 1
FT DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 47 1 (POTENTIAL).
FT DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 80 2 (POTENTIAL).
FT DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 98 118 3 (POTENTIAL).
FT DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 138 159 4 (POTENTIAL).
FT DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 263 6 (POTENTIAL).
FT DOMAIN 264 282 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 283 302 7 (POTENTIAL).
FT DOMAIN 303 >346 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 1 1 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 95 173 POTENTIAL.
FT NON_TER 346 346
SQ SEQUENCE 346 AA; 37986 MW; 97D3D7F45439BBD2 CRC64;
Query Match 67.4%; Score 1225.5; DB 1; Length 346;
Best Local Similarity 68.6%; Pred. No. 7e-64;
Matches 238; Conservative 35; Mismatches 73; Indels 1; Gaps 1;
4 NFSPLNEYEVESAGYTVLRILPLVGLVTVGLVGLNGLVWVAGFRMTRVTTC 63
1 NSSLPNISGGTPAVSAGYLFIDITVLFVAVTVGLVGLNGLVWVAGFRMTRVTTC 60

```

QY 64 YLNALADFSFATLPFLIVSMAMGEKWPFGWFLCKLHIHVVDINLFGSVFLGFIADLR 123
 DDb 61 YLNLAADFCSTSLPFFVWKAMGGHWPFGWFLCKFTFTIVDINLFGSVFLGFIADLR 120
 QY 124 CICVLHPVWQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPGNDTYCTFNFAW 183
 DDb 121 CVCVLHPVWQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPGNDTYCTFNFAW 180
 QY 184 GGTPEERLKVATMLTARGIRFVIGFSLPMSIVAICGLIAAKIHKMGKSSRPLRVL 243
 DDb 181 TNDPKERINVAIAMLTVGGIIRFIIGFSAPMSIVAVSYGLIATKIHKQGLKFSRPLRVL 240
 QY 244 TAVVASFFICWFPOLVALLGVTKMLFYCKYKIIIDILVNPSSLAFFNSCLNPMLYV 303
 DDb 241 SFVAAAFCLWSPQVQVAFIATVIRELL-OGMYKEIGIAVDVTSALAFFNSCLNPMLYV 299
 QY 304 FVGQDFRERLIHSLPTSLSERALSSEDAPTNDTAANSAPPAETELQA 350
 DDb 300 FMGQDFRERLIHSLPASLERALTEASTQTSATNSTLPSAEVALQA 346

RESULT 14
 FMLR_PONPY
 ID FMLR_PONPY STANDARD; PRT; 346 AA.
 AC P79235;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE fMet-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)
 DE (FPR) (N-formylpeptide chemoattractant receptor) (Fragment).
 GN FPR1.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96421539; PubMed=8824156;
 RA Alvarez V., Coto E., Shen F., Gouzalet-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in
 RT non-human primates";
 RL Immunogenetics 44:446-452(1996).
 CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,
 CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
 CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; X97735; CAA66319.1;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm1.1;
 CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1;
 CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2;
 CC K protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.
 CC NON_TER 1 1
 CC DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 25 47 1 (POTENTIAL).
 CC DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 59 80 2 (POTENTIAL).
 CC DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 98 118 3 (POTENTIAL).
 CC FT

FT DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 138 159 4 (POTENTIAL).
 FT DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 203 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 263 6 (POTENTIAL).
 FT DOMAIN 264 282 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 283 302 7 (POTENTIAL).
 FT DOMAIN 303 >346 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 1 1 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 95 173 POTENTIAL.
 FT NON_TER 346 346
 SQ SEQUENCE 346 AA; 38038 MW; A012B86BAA7B315 CRC64;

Query Match 67.4%; Score 1225.5; DB 1; Length 346;
 Best Local Similarity 68.9%; Pred. NO. 7e-64;
 Matches 239; Conservative 34; Mismatches 73; Indels 1; Gaps 1;

QY 4 NFSTPLNEYEVSYESAGTYVLRILPLVGLVGVTFVGLVGNGLVIVWAGFRMTRVTTIC 63
 DDb 1 NSSLEPTNISGGTPAVSAGYLFDIITYLVAVTFVGLVGNGLVIVWAGFRMTRVTTIS 60
 QY 64 YLNALADFSFATLPFLIVSMAMGEKWPFGWFLCKLHIHVVDINLFGSVFLGFIADLR 123
 DDb 61 YLNLAADFCSTSLPFFVWKAMGGHWPFGWFLCKFTFTIVDINLFGSVFLGFIADLR 120
 QY 124 CICVLHPVWQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPGNDTYCTFNFAW 183
 DDb 121 CVCVLHPVWQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPGNDTYCTFNFAW 180
 QY 184 GGTPEERLKVATMLTARGIRFVIGFSLPMSIVAICGLIAAKIHKMGKSSRPLRVL 243
 DDb 181 TNDPKERINVAIAMLTVGGIIRFIIGFSAPMSIVAVSYGLIATKIHKQGLKFSRPLRVL 240
 QY 244 TAVVASFFICWFPOLVALLGVTKMLFYCKYKIIIDILVNPSSLAFFNSCLNPMLYV 303
 DDb 241 SFVAAAFCLWSPQVQVAFIATVIRELL-OGMYKEIGIAVDVTSALAFFNSCLNPMLYV 299
 QY 304 FVGQDFRERLIHSLPTSLSERALSSEDAPTNDTAANSAPPAETELQA 350
 DDb 300 FMGQDFRERLIHSLPASLERALTEASTQTSATNSTLPSAEVALQA 346

RESULT 15
 FMLR_RABIT
 ID FMLR_RABIT STANDARD; PRT; 352 AA.
 AC Q05394;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE fMet-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)
 DE (FPR) (N-formylpeptide chemoattractant receptor).
 GN FPR1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-New Zealand white; TISSUE-Neutrophils;
 RX MEDLINE=93163563; PubMed=8432984;
 RA Ye R.D., Quehenberger O., Thomas K.M., Navarro J., Cavanagh S.L.,
 RA Prossnitz E.R., Cochran C.G.;
 RT "The rabbit neutrophil N-formyl peptide receptor. cDNA cloning,
 RT expression, and structure/function implications";
 RT J. Immunol. 150:1383-1394(1993)
 CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,
 CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
 CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC

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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:17:02 ; Search time 34 Seconds

(without alignments)
2127.133 Million cell updates/sec

Title: US-09-944-807-2

Perfect score: 1817

Sequence: 1 METNFTPLNEVEVSYESA.....TNDTAANSASPAETELQAM 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phase.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_rvirus.*
- 17: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1420	78.2	351	11	O88536
2	1325	72.9	347	11	O88535
3	1140.5	62.8	343	11	O88537
4	1107.5	61.0	323	11	O88538
5	549.5	30.2	475	11	O90WG9
6	500	27.5	355	6	Q95LH1
7	457.5	25.2	359	13	Q9PVY7
8	433	23.8	353	13	Q93247
9	427.5	23.5	359	6	Q9GLN9
10	426.5	23.5	359	4	O8TSK4
11	423.5	23.3	359	11	Q9EPP3
12	422.5	23.3	347	6	Q9MZM5
13	421.5	23.2	347	6	Q9MZP1
14	421.5	23.2	352	6	Q9TSQ8
15	421	23.2	347	6	Q9MZP3
16	421	23.2	347	6	Q9MZM1

17	420.5	23.1	334	6	O9N1P4
18	420.5	23.1	347	6	O9MQQ3
19	420.5	23.1	347	6	O9MQQ2
20	420.5	23.1	347	6	O9MQQ1
21	420.5	23.1	347	6	O9MQQ0
22	420.5	23.1	347	6	O9MZP9
23	420.5	23.1	347	6	O9MZP8
24	420.5	23.1	347	6	O9MZP5
25	420.5	23.1	347	6	O9MZP4
26	420.5	23.1	347	6	O9MZP2
27	420.5	23.1	347	6	O9MZP0
28	420.5	23.1	347	6	O9MZN9
29	420.5	23.1	347	6	O9MZN8
30	420.5	23.1	347	6	O9MZN7
31	420.5	23.1	347	6	O9MZM9
32	420.5	23.1	352	6	O77488
33	420	23.1	359	6	O9N0U1
34	419.5	23.1	347	6	O9MZN6
35	419.5	23.1	347	6	O9MZN5
36	419.5	23.1	347	6	O9MZN2
37	419.5	23.1	347	6	O9MZN1
38	419.5	23.1	358	13	O9YGC3
39	418.5	23.0	334	6	O9N130
40	418.5	23.0	347	6	O9MZP7
41	418.5	23.0	347	6	O9MZN4
42	418.5	23.0	347	6	O9MZN3
43	417.5	23.0	334	6	O9N1P2
44	417.5	23.0	357	13	O42445
45	417.5	23.0	359	11	O9EQR9

ALIGNMENTS

RESULT 1

ID	O88536	PRELIMINARY;	PRT;	351 AA.
AC	O88536;			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	N-formylpeptide receptor-like 2.			
GN	FPR-RS2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98390190; PubMed=9722950;			
RA	Gao J.-L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.;			
RT	"Differential expansion of the N-formylpeptide receptor gene cluster in human and mouse."			
RL	Genomics 51:270-276(1998).			
DR	EMBL; AF071180; AAC34585.1; -			
DR	MGI; MGI:1278319; Fpr-rs2.			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPS.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL1; UNKNOWN_1.			
DR	PROSITE; PS0262; G_PROTEIN_RECEP_FL2; 1.			
KW	Receptor.			
SQ	SEQUENCE 351 AA; 39422 MW; B16BCE7FA9AA8F43 CRC64;			

Query Match	78.2%	Score 1420;	DB 11;	Length 351;
Best Local Similarity	76.3%	Pred. No. 1.6e-115;		
Matches 267;	Conservative 33;	Mismatches 50;	Indels 0;	Gaps 0;
Qy	1	METNFTPLNEVEVSYESAGYVLRILPLVVLGVTFVLVGLNGLVWAGFRMTRTVT	60	
Db	1	MESNYSIHLNGSEVVYDSTISRLVILSMVVSITFLVGLNGLVWAGFRMPTVT	60	
Qy	61	TICYNLALADFSATLPLFLIVSNAMGEKWPFGWFLCKLIHVVDINLFGSVFLIGFIA	120	

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Db 61 TIWYLNALADFSFTATLPFLVEMAKKWPFGWFLCKLVHIVVDVNLFGSVFLIALIA 120
QY 121 LDRICVCLHPVMAQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPNGDYCTFNF 180
Db 121 LDRICVCLHPVMAQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPNGDYCTFNF 180
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKGMIKSSRPL 240
Db 181 GSAQTDEEKNLTAFTTTRGIIIRFLGFSMPMSIVAVCYGLIAVKNRNLNRRSL 240
QY 241 RVLTAVASFFICWPFQVLPVGLVWLMKEMFYGKYIIDILVNPSTSLAFFNSCLNPM 300
Db 241 RVLTAVASFFICWPFQVLPVGLVWLMKEMFYGKYIIDILVNPSTSLAFFNSCLNPM 300
QY 301 LYVFGQDFRRLIHSPTSLSERALSSEDAPTNDTAANSASPPAETELQA 350
Db 301 LYVFGQDFRRLIHSPTSLSERALSSEDAPTNDTAANSASPPAETELQA 350
RESULT 2
ID O88535 PRELIMINARY; PRT; 347 AA.
AC O88535;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE N-formylpeptide receptor-like 1.
GN FPR-RS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390190; PubMed=9722950;
RA Gao J.-L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.;
RT "Differential expansion of the N-formylpeptide receptor gene cluster
in human and mouse.";
RL Genomics 51:270-276(1998).
DR EMBL; AF071179; AAC34584.1; -.
DR MGD; MGI:1278320; Fpr-rs1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR01559; DUFFYANTIGEN.
DR PROSITE; PS00237; GPCRRHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL2; 1.
KW Receptor.
SQ SEQUENCE 347 AA; 39071 MW; A755BF9F09575A70 CRC64;
Query Match 72.9%; Score 1325; DB 11; Length 347;
Best Local Similarity 73.2%; Pred. No. 2.8e-107;
Matches 257; Conservative 27; Mismatches 63; Indels 4; Gaps 1;
QY 1 METNFTPLNEEVEVSAGYTVLRILPLVGLVTVFTVGLVGLVGLVWAGFRMTRVT 60
Db 1 METNFTPLNEEVEVSAGYTVLRILPLVGLVTVFTVGLVGLVGLVWAGFRMTRVT 60
QY 61 TICVNLALADFSFTATLPFLVEMAKKWPFGWFLCKLVHIVVDVNLFGSVFLIALIA 120
Db 61 TICVNLALADFSFTATLPFLVEMAKKWPFGWFLCKLVHIVVDVNLFGSVFLIALIA 120
QY 121 LDRICVCLHPVMAQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPNGDYCTFNF 180
Db 121 LDRICVCLHPVMAQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPNGDYCTFNF 180
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKGMIKSSRPL 240
Db 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKGMIKSSRPL 240
QY 241 RVLTAVASFFICWPFQVLPVGLVWLMKEMFYGKYIIDILVNPSTSLAFFNSCLNPM 300
Db 241 RVLTAVASFFICWPFQVLPVGLVWLMKEMFYGKYIIDILVNPSTSLAFFNSCLNPM 300
QY 301 LYVFGQDFRRLIHSPTSLSERALSSEDAPTNDTAANSASPPAETELQA 350
Db 301 LYVFGQDFRRLIHSPTSLSERALSSEDAPTNDTAANSASPPAETELQA 350
RESULT 4
ID O88538 PRELIMINARY; PRT; 323 AA.
AC O88538;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
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Db 237 RVLTAVASFFICWPFQVLPVGLVWLMKEMFYGKYIIDILVNPSTSLAFFNSCLNPM 296
QY 301 LYVFGQDFRRLIHSPTSLSERALSSEDAPTNDTAANSASPPAETELQA 351
Db 297 LYVFGQDFRRLIHSPTSLSERALSSEDAPTNDTAANSASPPAETELQA 347
RESULT 3
ID O88537 PRELIMINARY; PRT; 343 AA.
AC O88537;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE N-formylpeptide receptor-like 3.
GN FPR-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390190; PubMed=9722950;
RA Gao J.-L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.;
RT "Differential expansion of the N-formylpeptide receptor gene cluster
in human and mouse.";
RL Genomics 51:270-276(1998).
DR EMBL; AF071181; AAC34586.1; -.
DR MGD; MGI:1278318; Fpr-rs3.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRRHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL2; 1.
KW Receptor.
SQ SEQUENCE 343 AA; 38111 MW; 0F726BF195CBFB29 CRC64;
Query Match 62.8%; Score 1140.5; DB 11; Length 343;
Best Local Similarity 65.2%; Pred. No. 3.1e-91;
Matches 227; Conservative 38; Mismatches 78; Indels 5; Gaps 1;
QY 1 METNFTPLNEEVEVSAGYTVLRILPLVGLVTVFTVGLVGLVGLVWAGFRMTRVT 60
Db 1 METNFTPLNEEVEVSAGYTVLRILPLVGLVTVFTVGLVGLVGLVWAGFRMTRVT 60
QY 61 TICVNLALADFSFTATLPFLVEMAKKWPFGWFLCKLVHIVVDVNLFGSVFLIALIA 120
Db 61 TICVNLALADFSFTATLPFLVEMAKKWPFGWFLCKLVHIVVDVNLFGSVFLIALIA 120
QY 121 LDRICVCLHPVMAQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPNGDYCTFNF 180
Db 121 LDRICVCLHPVMAQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPNGDYCTFNF 180
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKGMIKSSRPL 240
Db 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKGMIKSSRPL 240
QY 241 RVLTAVASFFICWPFQVLPVGLVWLMKEMFYGKYIIDILVNPSTSLAFFNSCLNPM 300
Db 241 RVLTAVASFFICWPFQVLPVGLVWLMKEMFYGKYIIDILVNPSTSLAFFNSCLNPM 300
QY 301 LYVFGQDFRRLIHSPTSLSERALSSEDAPTNDTAANSASPPAETELQA 348
Db 296 LYVFGQDFRRLIHSPTSLSERALSSEDAPTNDTAANSASPPAETELQA 343
RESULT 4
ID O88538 PRELIMINARY; PRT; 323 AA.
AC O88538;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
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DE N-formylpeptide receptor-like 4.
GN FPR-RS4
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390190; PubMed=9722950;
RA Gao J.-L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.;
RT "Differential expansion of the N-formylpeptide receptor gene cluster
in human and mouse."
RL Genomics 51:270-276(1998).
DR EMBL: AF011182; AAC34587.1; -
DR MGD; MGI:1278317; Fpr-rs4. GPCR_Rhodpsn.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1559; DUFFYANTIGEN.
DR PRINTS; PRO0237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
DR Receptor.
SQ SEQUENCE 323 AA; 36299 MW; CC90EC09B4725036 CRC64;
Query Match 61.0%; Score 1107.5; DB 11; Length 323;
Best Local Similarity 65.5%; Pred. No. 2.1e-88;
Matches 215; Conservative 39; Mismatches 69; Indels 5; Gaps 1;
QY 1 MEVNFSTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVLGNGLVWVAGFRMTRVT 60
DB 1 MEVNISPLNGSEVVFYDSTSSVLTSLVLFITFVLGVLGNGLVWVAGFQMAHTVT 60
QY 61 TICVNLALADFSFATLPLPLIVSMANGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
DB 61 TVSYNLALSDLSFVWFLPLPHIISVWVRGKFLGFLCKLVHIANLNFVSFLITLIA 120
QY 121 LDRICVLPVWVAQNHTVSLAMKVIVGVPWILALVLTLPVFLFTVTTPNGDTCYCFNF 180
DB 121 MDRICVLPVWVAQNHTVSLAMKVIVGVPWILALVLTLPVFLFTVTTPNGDTCYCFNF 180
QY 181 ASNGGTPEERLKVATMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMKSSRPL 240
DB 181 ESWVATSEQLKMSVIAATASGIINFTIGFSPMSFATCYGLMAAKICRRGFVNSSRPL 240
QY 241 RVLTAVVASFICWFPPQVALLGTWVKEMLFYGYKIIDILVNPSTSSLAFFNSCLNPM 300
DB 241 RVLTAVVASFICWFPPQVALLGTWVKEMLFYGYKIIDILVNPSTSSLAFFNSCLNPM 300
QY 301 LVYFVGQDFRERLIHSLPTSLERALSSED 328
DB 296 LVYFVGQDFRERLIHSLPTSLERALSSED 323
RESULT 5
Q9QW9 PRELIMINARY; PRT; 475 AA.
ID Q9QW9
AC Q9QW9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anaphylatoxin C3a receptor.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HARTLEY; TISSUE=SPLN;
RX MEDLINE=98414293; PubMed=9743361;
RA Fukuoka Y., Ember J.A., Hugli T.E.;
RT "Molecular cloning of two isoforms of the guinea pig C3a anaphylatoxin
receptor: alternative splicing in the large extracellular loop."
RL J. Immunol. 161:2977-2984(1998).

DR EMBL: U86378; AAC36503.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
DR Receptor.
SQ SEQUENCE 475 AA; 53528 MW; 2C2C4D6C02170726 CRC64;
Query Match 30.2%; Score 549.5; DB 11; Length 475;
Best Local Similarity 28.8%; Pred. No. 1e-39;
Matches 136; Conservative 61; Mismatches 104; Indels 171; Gaps 10;
QY 2 ETNFSTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVLGNGLVWVAGFRMTRVT 61
DB 7 ETN-STGLHLEPQYQPET-----ILAMAILGLTFLVGLPGNGLVWVAGLKKMRRTVNT 58
QY 62 ICVNLALADFSFATLPLPLIVSMANGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIAL 121
DB 59 VWFLHLTVADFVCCLSLPSMAHLALRGYPYGEILCKFTPTVIFNMFASVFLITLISL 118
QY 122 DRICVLPVWVAQNHTVSLAMKVIVGVPWILALVLTLPVFLFTVTTPNGDTCYCFNF 181
DB 119 DRCLMVLKPIWQNHNRVNTACIICGICILVAVFLCIPVFVYRETFTLEN-HTICTYFNS 177
QY 182 -----SWG-GTP----- 187
DB 178 PGSFYLDYAYDRDAGYGTDPDPIVQLPGEMEHRSDSPSFQTDGPMWSTTLYTSQSR 237
QY 188 --BERLKVAITMTARG----- 202
DB 238 PSEDSFMDSAKLSGQGYVDVLPVLTNLCGLPMEENTNTLHNAAFSLSSDLVDVSNATQC 297
QY 203 -----IIRFVIGFSLPMSIVAICYGLIAAKIHK 231
DB 298 LSTPEPQDFWDDLSPTFHEVTRPLKVTFTLRVWGLLPMIIVACVTLIIFRMRRA 357
QY 232 GMKS-SRPLRVLTAVVASFICWFPPQVALLGTWVKEMLFYGYKIIDILVNPSTSS 288
DB 358 RVKSNWNLKHLAMVVVTFILICWAPYH-----FGVILFINPESRV 400
QY 289 -----SLAFNSCLNPMLYVFGQDFRERLIHSLPTSLERALSSED 328
DB 401 GAALLSDHVSIALASANSFNPFLYALLGLRKRVRQSMKKGLEAASED 452
RESULT 6
Q95LH1 PRELIMINARY; PRT; 355 AA.
ID Q95LH1
AC Q95LH1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE G protein-coupled receptor 1.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Wade-Evans A.M., Javan C., Russell J., Jenkins A.;
RT "Cloning and sequencing of simian G-protein coupled receptors, which
may function as SIV/SHIV co-receptors, from cynomolgus macaque
PBMCs."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF292382; AAK97052.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
DR Receptor.
SQ SEQUENCE 355 AA; 41370 MW; 1DDE41BE9CAC525C CRC64;

Query Match		27.5%;	Score 500;	DB 6;	Length 355;
Best Local Similarity		33.0%;	Pred. No. 1.5e-35;		
Matches 114;		Conservative	69;	Mismatches 132;	Indels 30; Gaps 7;
QY	1	MTNFSTPLNEEYVS	-----ESAGTIVLRILPLVLGVTFVLGVLNGLVI	48	
DB	1	MEDLEETLFEFENYS	ALDYSLDESLEEKVQGVHWSLVLYCLSFVLGIPGNAIV	60	
QY	49	WVAGFRWTRVTITIC	YALALADSFATPLPLVISMAMGKWPFGWFLCKLIHIVDIN	108	
DB	61	WFTGFKWRTVSTLW	FLNALADIFLFLPLYSIVYVYVNFHWPFGIWLCKANSFTAQIN	120	
QY	109	LEGSVLLGFETALDC	ICVLPVMAQNHRTVSLAMKVIVGVWILALVTLPLVFLFTVT	168	
DB	121	MFASVFFTVISLDH	YIHLHPVLSHRRTLKNSLIVIFILWLLSGGALYFRDTVE	180	
QY	169	IPNGDTYCTFNFAWG	PTPEERLKVATMLTARGI--IRFVIGFSLPMSIVAICYGLIAA	226	
DB	181	F--NNHTLCYNF	-----QKHDPLTVIRHHVLTWVKYIVGYLFLPLTMSICYLCIL	231	
QY	227	KHKGMKMSRPLRLV	LTAJVASFICWFPQVLVALLGVWLMKMLFYGKYK--IIDLIV	284	
DB	232	KVKRSILISSRHFHT	ETILAVVAFVVCWTPVHLF-----SIW-ELTIHNSYSHVYMAQGI	286	
QY	285	NPTSLAFENCLNPL	MLYVFGQDFRERLIHSLPTSLERALSDDS	329	
DB	287	PLSTGLAFENCLNP	ILYVLISKFKQARFSSVAEILKYTLWEVS	331	
RESULT 7					
Q9PVY7					
ID	Q9PVY7	PRELIMINARY;	PRT;	359 AA.	
AC	Q9PVY7;				
DT	01-MAY-2000	(Tremblrel. 13, Created)			
DT	01-MAY-2000	(Tremblrel. 13, Last sequence update)			
DT	01-MAR-2002	(Tremblrel. 20, Last annotation update)			
DE	Angiotensin receptor.				
OS	Anguilla anguilla	(European freshwater eel).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;				
OC	Anguilla.				
OX	NCBI_TaxID=7936;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Tran Van Chuoi M., Dolphin C.T., Barker S., Clark A.J., Vinson G.P.;				
RA	"Molecular cloning and characterization of the cDNA encoding the				
RT	angiotensin II receptor of european eel Anguilla anguilla."				
RT	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.				
RL	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL; AJ005132; CAB40835.1; -.				
DR	HSSP; P34996; 1DDD.				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR000130; 2n_MTPeptide.				
DR	Pfam; PF00001; 7tm.1; 1.				
DR	PRINTS; PR00237; GPCRHHODPSN.				
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.				
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.				
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.				
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.				
QY	SEQUENCE	359 AA;	39997 MW;	053726A827C271	CRC64;
Query Match					
Best Local Similarity		25.2%;	Score 457.5;	DB 13;	Length 359;
Matches 119;		Conservative	34.7%;	Pred. No. 7.6e-32;	
			59;	Mismatches 126;	Indels 39; Gaps 10;
QY	24	VLRLPLVLVGLVTFV	LGVLGVLGIWIVA-GFRWTRVTITICYNLALADSFATLPLFI	82	
DB	25	IYTLIP-VVYGCNFI	VIGVIGNSVAVIYCYMKIKLVANIFVLNLAVALSDTLFLITLPMAW	83	
QY	83	VSMAMGKWPFGWFL	CKLIHIVDINLFGSVFLIGFIALDRCICVLPVMAQNHRTVSLA	142	

Ddb	84	TTTAMGYNWPGGFLCKASAGITIFNLTSISFFLTSIDRYLAIVHPVRSQRRTVVYA	143
Qy	143	MKVIVGPMILALVPLPVFLFTVTI--PNGDTYCTFNFAWGSGTPEERLKVATMLTA	200
Ddb	144	RITCVLIWAFALSLPTALSROVFTIHPN-TTVC-----GTLDKHEL---HVLVA	192
Qy	201	RGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKISSRP-----LRVLTAVVASFFICWF	255
Ddb	193	IGLMSVLGFLPIFVIIIVTVCYCLIGRALLARRVQSSRSRGDEVQLMLAAVVAFLFCWV	252
Qy	256	PFQVALLGTV-WKEMLFYKGYKIITILVNPTSSLAFFENCLNPMLYVFGQDFRRLI	314
Ddb	253	PHQIFHMHVLAUKLVENCPDLDIIDTALPFTICIAVFNSCMNPILYGFVGRNFRNLL	312
Qy	315	-----HSLP-----TSLERALSEDSAPTNDTAANS	339
Ddb	313	RLRCGPGSAAHSHPSLTTKMTSLSYRASETRLTSLGKAASS	355
RESULT 8			
Q93247			
ID	Q93247	PRELIMINARY;	PRT; 353 AA.
AC	Q93247;		
DT	01-NOV-1998	(Tremblrel. 08, Created)	
DT	01-NOV-1998	(Tremblrel. 08, Last sequence update)	
DT	01-JUN-2002	(Tremblrel. 21, Last annotation update)	
DE	CXCR4.		
OS	Cyprinus carpio	(Common carp).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Cyprinus.		
OX	NCBI_TaxID=7962;		
RN	[1]		
RA	SEQUENCE FROM N.A.		
RP	MEDLINE-99367403; PubMed-10436187;		
RR	Fujiki K., Shin D., Nakao M., Yano T.;		
RRX	"Molecular cloning of carp (Cyprinus carpio) CC chemokine, CXCR4		
RT	chemokine receptors, allograft inflammatory factor-1, and natural		
RT	killer cell enhancing factor by use of suppression subtractive		
RT	hybridization."		
RRL	Immunogenetics 49:909-914(1999).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	EMBL; AB012310; BAA32797.1; -.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF000001; 7tm.1; 1.		
DR	PRINTS; PR01558; CHEMOKINER11.		
DR	PRINTS; PR00237; GPCRHHODPSN.		
DR	PRINTS; PR01568; LYMPHOTACTNR.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.		
DR	G-protein coupled receptor; Glycoprotein; Transmembrane.		
MSK	SEQUENCE 353 AA; 39633 MW; 84924BE413FB3B3F CRC64;		
Query Match			
Best Local Similarity		23.8%;	Score 433; DB 13; Length 353;
Matches 112; Conservative		31.5%;	Pred. No. 1e-29;
		66;	Mismatches 114; Indels 64; Gaps
Qy	10	NEYEEVSEYAGYVLRILPLVVLGVTFVLGVLGVLGIWVAGF-RMTRVTITICYNLA	68
Ddb	32	NDFQKI-----FLP-VVYGIIFVLGIINGLVLMVGMFGKSKNMTDKYRLHLS	79
Qy	69	LADFSFTATLPFLIVSMAMGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVL	128
Ddb	80	IADLLFVLTPFWAVDAASG--WHEGGFLCVTVNMITYLNLYSSVLLIAFLISLDRIYAV	137
Qy	129	HPVMAQNHRTVSLAMKVI-VGPWILALVTLPLVFLFTVTIPNGDTYCTFNFAWGSGTP	187
Ddb	138	RATNSQNFRRY-LAEKVILGVWLPASLLTPDLVF-AKVHDTGMNTICELTYPLQGTN-	194
Qy	188	EERLKVAITMLTARGIIRF---VIGFSLPMSIVAICYGLIAAKIHK--KGMKISSRPLRV	242


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Db 195 -----VKAVERFQHFVGFLLPGLLIILTCYCIILSKSKSGQALKRKALKT 243
Qy 243 LTAVVASFFICWFQFQVALLGTV-----WLKEMLFYGYKYKIIDIILVNPTS 288
Db 244 TVIILLCFFICWLYCAGILVDITLMLNLSHTCFLEQLEKWIFF-----TE 291
Qy 289 SLAFFNSCLNMLVVFVQDPRERLIHSL---PTSLERALSSEDSAPTNDTAANSAS 341
Db 292 ALAYFHCLNPLILYAFVGVKESKARNALSISRSSHMLTKKRGPISSVSTESSES 347

RESULT 9
Q9GLN9 PRELIMINARY; PRT; 359 AA.
AC Q9GLN9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Angiotensin II type-1 receptor.
GN AGRI1.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469400; Pubmed=11013071;
RA DuFour C., Casane D., Denton D., Wickings J., Corvol P.,
RA Jeunemaitre X.;
RT "Human-Chimpanzee DNA sequence variation in the four major genes of
RT the renin angiotensin system.";
RL Genomics 69:14-26(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF193445; AAG28410.1; -.
DR HSSP; P34996; 1DDO.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PRO0237; GPCRRHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41033 MW; 266133A7A3E911A6 CRC64;

Query Match 23.5%; Score 427.5; DB 6; Length 359;
Best Local Similarity 31.0%; Pred. No. 3.1e-29;
Matches 103; Conservative 69; Mismatches 123; Indels 37; Gaps 9;

Qy 35 VTFVLGVLGGLVIVVAGFRM-TRVTTCYLNALADFSFATLPLFLIVSMAMGEKWP 93
Db 37 IIFVVGIFGNSLVIVYFYMKLTVASVFLNLALADLCFLLLPLWAVYTAMEYRWPF 96
Qy 94 GWFLCKLHIHVVNINLFGSVFLIGFIALDRICVLHPVWQNHRTVSLAMKVIVGPMILA 153
Db 97 GNYLCKIASASVSNLYASVELLCTLSIDRYLAIVHPMKSLRRTMLVAKVTCIIWLLA 156
Qy 154 LVLPVLPVLFVTTIPNGD-TYCTFNPSWGGTPEERLKVATMLTARGIIRFVIGFSL 212
Db 157 GLASLPALIHNRVFFIENTNITVCAFYHESQNST---LPGL-----GLTKNIGLFL 206
Qy 213 PMSIVAICYGLIAAKIHKKGKSRP-----LRVLTAVASFFICWFQFQVALLGTVW 267
Db 207 PFLIILTYSYTLWAKKAYEQKNKPRNDDIFKIIAIVLFFFSWIPHQIFTLFDV-- 264
Qy 268 LKEMLFYGYKYK-----IIDILVNPTSLAFNSCLNMLVVFVQDPRF---RLIHS 318
Db 265 ---LIQLGIIRDCTADIVDTAMPITICIAFNCLNPLFVGLGKKEKFLQLLKVIP 321
Qy 319 -----TSLERALSSEDSAPTNDTAANSASPPA 344
Db 322 PKAKSHSNLSTKMSLTSLYRSDNVSSSTKKPA 353

Qy 35 VTFVLGVLGGLVIVVAGFRM-TRVTTCYLNALADFSFATLPLFLIVSMAMGEKWP 93
Db 37 IIFVVGIFGNSLVIVYFYMKLTVASVFLNLALADLCFLLLPLWAVYTAMEYRWPF 96
Qy 94 GWFLCKLHIHVVNINLFGSVFLIGFIALDRICVLHPVWQNHRTVSLAMKVIVGPMILA 153
Db 97 GNYLCKIASASVSNLYASVELLCTLSIDRYLAIVHPMKSLRRTMLVAKVTCIIWLLA 156
Qy 154 LVLPVLPVLFVTTIPNGD-TYCTFNPSWGGTPEERLKVATMLTARGIIRFVIGFSL 212
Db 157 GLASLPALIHNRVFFIENTNITVCAFYHESQNST---LPGL-----GLTKNIGLFL 206
Qy 213 PMSIVAICYGLIAAKIHKKGKSRP-----LRVLTAVASFFICWFQFQVALLGTVW 267
Db 207 PFLIILTYSYTLWAKKAYEQKNKPRNDDIFKIIAIVLFFFSWIPHQIFTLFDV-- 264
Qy 268 LKEMLFYGYKYK-----IIDILVNPTSLAFNSCLNMLVVFVQDPRF---RLIHS 318
Db 265 ---LIQLGIIRDCTADIVDTAMPITICIAFNCLNPLFVGLGKKEKFLQLLKVIP 321
Qy 319 -----TSLERALSSEDSAPTNDTAANSASPPA 344
Db 322 PKAKSHSNLSTKMSLTSLYRSDNVSSSTKKPA 353

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RESULT 10
Q8TBK4 PRELIMINARY; PRT; 359 AA.
AC Q8TBK4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Angiotensin receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022447; AAH22447.1; -.
KW Receptor.
SQ SEQUENCE 359 AA; 41087 MW; AF90BE7F21E911BA CRC64;

Query Match 23.5%; Score 426.5; DB 4; Length 359;
Best Local Similarity 31.0%; Pred. No. 3.8e-29;
Matches 103; Conservative 68; Mismatches 124; Indels 37; Gaps 9;

Qy 35 VTFVLGVLGGLVIVVAGFRM-TRVTTCYLNALADFSFATLPLFLIVSMAMGEKWP 93
Db 37 IIFVVGIFGNSLVIVYFYMKLTVASVFLNLALADLCFLLLPLWAVYTAMEYRWPF 96
Qy 94 GWFLCKLHIHVVNINLFGSVFLIGFIALDRICVLHPVWQNHRTVSLAMKVIVGPMILA 153
Db 97 GNYLCKIASASVSNLYASVELLCTLSIDRYLAIVHPMKSLRRTMLVAKVTCIIWLLA 156
Qy 154 LVLPVLPVLFVTTIPNGD-TYCTFNPSWGGTPEERLKVATMLTARGIIRFVIGFSL 212
Db 157 GLASLPALIHNRVFFIENTNITVCAFYHESQNST---LPGL-----GLTKNIGLFL 206
Qy 213 PMSIVAICYGLIAAKIHKKGKSRP-----LRVLTAVASFFICWFQFQVALLGTVW 267
Db 207 PFLIILTYSYTLWAKKAYEQKNKPRNDDIFKIIAIVLFFFSWIPHQIFTLFDV-- 264
Qy 268 LKEMLFYGYKYK-----IIDILVNPTSLAFNSCLNMLVVFVQDPRF---RLIHS 318
Db 265 ---LIQLGIIRDCTADIVDTAMPITICIAFNCLNPLFVGLGKKEKFLQLLKVIP 321
Qy 319 -----TSLERALSSEDSAPTNDTAANSASPPA 344
Db 322 PKAKSHSNLSTKMSLTSLYRSDNVSSSTKKPA 353

RESULT 11
Q9EPP3 PRELIMINARY; PRT; 359 AA.
AC Q9EPP3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
GN ATI.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GALL BLADDER;
RA Busmann A., Noack T., Zucht HD., Forssmann W.G., Meyer M.;
RT "Isolation of Angiotensin I from human hemofiltrate as a potent
RT modulator of KATP channels.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ301623; CAC21550.1; -.

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QY 85 MAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRICVILHPWAQNHRTVSLAMK 144
DB 93 AV--ANNYFGNFCFLCKAVHVIYTVNLYSSVLLILAFISLDRLYLAVHATNSQKPKRL-LAEK 149
QY 145 VI-VGPMILALVTLPLVFLFLTTVT-----IPNGDTYCTFNFAWGGTPEERLKV 193
DB 150 VVYGVWIPALLTIPDFIFASVSEADDRFCDFRYPNDLWVVVFQFQ----- 197
QY 194 AITMLTARGIIRFVIGSLPMSIVAICYGLIAAKI-HKGMKISSRRLRVLTVAVASFFI 252
DB 198 -----HIMVGLILPGVILSCYIIISKLSHGKHQK-RKALKTTVILILAFFA 245
QY 253 CWFPFQVALLGTVWLKEMLFY-----KYKIIDLINVTSSLAFFNSCLNPMLYYFVG 306
DB 246 CWLPYIGISIDSFILLEIKQCEPENTVHKWISI-----TEALAFPHCCNLPILYAFLG 301
QY 307 QDFRERLIHSLPTSRLALS 326
DB 302 AKFKTSAQHAL-TSVSRGSS 320
RESULT 14
Q9TSQ8 PRELIMINARY; PRT; 352 AA.
AC Q9TSQ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE G-protein coupled receptor.
GN CXCR4.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Holtkamp N., Baier M., Warner A.;
RT "CXCR4 from African green monkey.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF019378; AD01638.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR01558; CHEMOKINER11.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01568; LYMPHOTACTNR.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 39624 MW; F240B686D5B368F CRC64;

Query Match 23.2%; Score 421.5; DB 6; Length 352;
Best Local Similarity 33.1%; Pred. No. 1e-28;
Matches 106; Conservative 56; Mismatches 107; Indels 51; Gaps 11;

QY 26 RILPLVVLGVTVFVLGVLGNGLVIVWAGF-RMTRVTTCVILNLAALDFSTATLPFLIVS 84
DB 38 RIFLPITYSIIFLTGIVGNGLVILVMGYQKLRSMYDKYRLHLSVDALLFVITLPFWAVD 97
QY 85 MAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRICVILHPWAQNHRTVSLAMK 144
DB 98 AV--ANNYFGNFCFLCKAVHVIYTVNLYSSVLLILAFISLDRLYLAVHATNSQKPKRL-LAEK 154
QY 145 VI-VGPMILALVTLPLVFLFLTTVT-----IPNGDTYCTFNFAWGGTPEERLKV 193
DB 155 VVYGVWIPALLTIPDFIFASVSEADDRFCDFRYPNDLWVVVFQFQ----- 202
QY 194 AITMLTARGIIRFVIGSLPMSIVAICYGLIAAKI-HKGMKISSRRLRVLTVAVASFFI 252

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DB 203 -----HIMVGLILPGVILSCYIIISKLSHGKHQK-RKALKTTVILILAFFA 250
QY 253 CWFPFQVALLGTVWLKEMLFY-----KYKIIDLINVTSSLAFFNSCLNPMLYYFVG 306
DB 251 CWLPYIGISIDSFILLEIKQCEPENTVHKWISI-----TEALAFPHCCNLPILYAFLG 306
QY 307 QDFRERLIHSLPTSRLALS 326
DB 307 AKFKTSAQHAL-TSVSRGSS 325
RESULT 15
Q9MZP3 PRELIMINARY; PRT; 347 AA.
AC Q9MZP3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chemokine receptor CXCR4 (Fragment).
GN CXCR4.
OS Presbytis entellus (Human langur).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=9574;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF172220; AAF89340.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR01558; CHEMOKINER11.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01568; LYMPHOTACTNR.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 347 AA; 39145 MW; E96B660F1541515C CRC64;

Query Match 23.2%; Score 421; DB 6; Length 347;
Best Local Similarity 31.8%; Pred. No. 1.1e-28;
Matches 110; Conservative 59; Mismatches 115; Indels 62; Gaps 12;

QY 26 RILPLVVLGVTVFVLGVLGNGLVIVWAGF-RMTRVTTCVILNLAALDFSTATLPFLIVS 84
DB 33 RIFLPITYSIIFLTGIVGNGLVILVMGYQKLRSMYDKYRLHLSVDALLFVITLPFWAVD 92
QY 85 MAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRICVILHPWAQNHRTVSLAMK 144
DB 93 AV--ANNYFGNFCFLCKAVHVIYTVNLYSSVLLILAFISLDRLYLAVHATNSQKPKRL-LAEK 149
QY 145 VI-VGPMILALVTLPLVFLFLTTVT-----IPNGDTYCTFNFAWGGTPEERLKV 193
DB 150 VVYGVWIPALLTIPDFIFASVSEADDRFCDFRYPNDLWVVVFQFQ----- 197
QY 194 AITMLTARGIIRFVIGSLPMSIVAICYGLIAAKI-HKGMKISSRRLRVLTVAVASFFI 252
DB 198 -----HIMVGLILPGVILSCYIIISKLSHGKHQK-RKALKTTVILILAFFA 245
QY 253 CWFPFQVALLGTVWLKEMLFY-----KYKIIDLINVTSSLAFFNSCLNPMLYYFVG 306
DB 246 CWLPYIGISIDSFILLEIKQCEPENTVHKWISI-----TEALAFPHCCNLPILYAFLG 301
QY 307 QDFRERLIHSLPTSRLALS-----EDSAPTNDTAANSAS 341

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Db 302 AKFQTSQAHAL-TSVSRGSSILKILSKRGCHSVSTESSESSSHS 346

Search completed: December 16, 2002, 17:19:30
Job time : 36 secs

QY 61 TICYNLALADFSFATLPFLIVSAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120
 Db 61 TISYNLAVADECFSTLPFFVMVRAMGHWPFPGWFLCKFLFETVIDINLFGSVFLIALIA 120
 QY 121 LDRICVLPVWQAQNHRTVSLAMKVIVGPMILALVLTLPVFLFATVTPNGDTCYCTFNF 180
 Db 121 LDRICVLPVWQAQNHRTVSLAMKVIVGPMILALVLTLPVFLFATVTPNGDTCYCTFNF 180
 QY 181 ASWGTPPERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
 Db 181 SPWTDNPKRINVAAMLTVRGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
 QY 241 RVLTAVASFFICWPFQVALLGVWLMKEMLFYCKYKIIDLINPTSSLAFFNSCLNPM 300
 Db 241 RVLTAVASFFICWPFQVALLGVWLMKEMLFYCKYKIIDLINPTSSLAFFNSCLNPM 300
 QY 301 LYVFGQDFRERLIHALPASLERALTEDSTQTSATNSTLPSAEVALQA 349
 Db 301 LYVFGQDFRERLIHALPASLERALTEDSTQTSATNSTLPSAEVALQA 349

RESULT 2

US-08-430-286A-8
 ; Sequence 8, Application US/08430286A
 ; Patent No. 6225080

GENERAL INFORMATION:

APPLICANT: Uhl, George R.
 APPLICANT: Eppler, C. Mark
 APPLICANT: Wang, Jai-Bel
 TITLE OF INVENTION: Mu-Subtype Opioid Receptor
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Darby & Darby PC
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: US
 ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/430, 286A
 FILING DATE: 28-APR-1995
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Robinsop, Joseph R.
 REGISTRATION NUMBER: 33,448
 REFERENCE/DOCKET NUMBER: 0846/1A843-US5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-527-7700
 TELEFAX: 212-753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: F-PEP

US-08-430-286A-8

Query Match 68.3%; Score 1240.5; DB 4; Length 350;
 Best Local Similarity 68.6%; Pred. No. 1.4e-84;
 Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

QY 1 METNFSTPLNEYEVSYSAGYTVLRILPLVLVGLVGLNGLVWAGFRTRIVT 60

Db 1 METNSSLPTNIGGTPAVSAGYLFLODIITYLVFAVTVFVLVGLNGLVWAGFRTHRTVT 60
 QY 61 TICYNLALADFSFATLPFLIVSAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120
 Db 61 TISYNLAVADECFSTLPFFVMVRAMGHWPFPGWFLCKFLFETVIDINLFGSVFLIALIA 120
 QY 121 LDRICVLPVWQAQNHRTVSLAMKVIVGPMILALVLTLPVFLFATVTPNGDTCYCTFNF 180
 Db 121 LDRICVLPVWQAQNHRTVSLAMKVIVGPMILALVLTLPVFLFATVTPNGDTCYCTFNF 180
 QY 181 ASWGTPPERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
 Db 181 SPWTDNPKRINVAAMLTVRGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
 QY 241 RVLTAVASFFICWPFQVALLGVWLMKEMLFYCKYKIIDLINPTSSLAFFNSCLNPM 300
 Db 241 RVLTAVASFFICWPFQVALLGVWLMKEMLFYCKYKIIDLINPTSSLAFFNSCLNPM 300
 QY 301 LYVFGQDFRERLIHALPASLERALTEDSTQTSATNSTLPSAEVALQA 349
 Db 301 LYVFGQDFRERLIHALPASLERALTEDSTQTSATNSTLPSAEVALQA 349

RESULT 3

US-08-458-970A-10
 ; Sequence 10, Application US/08458970A
 ; Patent No. 5861272

GENERAL INFORMATION:

APPLICANT: LI, ET AL.
 TITLE OF INVENTION: C5a Receptor
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,970A
 FILING DATE: June 2, 1995
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09234
 FILING DATE: 16 AUG 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 325800-353
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-458-970A-10

Query Match 64.6%; Score 1174.5; DB 2; Length 364;
 Best Local Similarity 64.6%; Pred. No. 1.1e-79;
 Matches 237; Conservative 38; Mismatches 73; Indels 19; Gaps 5;

QY 1 METNFSTPLNEYE-----EVSYESAGYTVLRILPLVLVGLVGLVGLNGLVWAG 52

Db 1 MTNLSLLMKNSAVNLMMVSGTSQSVAGYIVLDVFSILFAVTVGLVGLNGLVIWAG 60
Qy 53 FRMTFTVTTICYNLALADFSATPLFLIIVSMAMGKWPFGWFLCKLIHVVVDINLFGS 112
Db 61 FRKHTVTTISYLNLAIDFCFTSTPLFYIASMMGHHWPGFWMCKFTYTVIDINLFGS 120
Qy 113 VFLIGFIALDRICICVLHPVMAQNHRTVSLAMKVIIVGPHILALVTLPLVFLFTVTPN- 171
Db 121 VFLIALIALDRICICVLHPVMAQNHRTVSLAMKVIIVGPHILALVTLPLVFLFTVTPN- 178
Qy 172 ---GDTYCTFNFAWSGCTPEERLKVATMLTARIIIFVIGFSLPMSIVAICYGLIAAK 227
Db 179 RLGPCKTACTDFSPWTKDPVEKRVAVTMLTVRGIIRFIFGTFSPMSIVAICYGLITK 238
Qy 228 IHKGMKSSRLRVLTAVASFFCWPFPQVALLGVTKEMLFYGYKYKIIDLIVNPT 287
Db 239 ITHROGLIKSSRLRVLTAVASFFCWPFPQVALLGVTKEMLFYGYKYKIIDLIVNPT 297
Qy 288 SSLAFNSCLNPLMVLVFGQDFRERLIHSLPTSLERALSSEDAPTNDTAAN---SASPPA 344
Db 298 SPLAFNSCLNPLMVLVFGQDFRERLIHSLPTSLERALSSEDAPTNDTAAN---SASPPA 357
Qy 345 ETELOAM 351
Db 358 ENTINAM 364

RESULT 4
US-08-118-270-34
; Sequence 34, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-34

Query Match 61.5%; Score 1117; DB 1; Length 315;
Best Local Similarity 67.3%; Pred. No. 1.7e-75;
Matches 218; Conservative 37; Mismatches 59; Indels 10; Gaps 4;
Qy 27 ILPLVVLGVTVFVLGVLNGLVIAWAGFRMTVTTICYNLALADFSATPLFLIIVSMA 86
Db 1 IITLVFAVRVFLGVLNGLVIAWAGFRMTVTTISYLNLAADFCFTSTLFFFWRLG 60
Qy 87 MGEKWPFGWFLCKLIHVVVDINLFGSVFLIGFIALDRICICVLHPVMAQNHRTVSLAMKVI 146
Db 61 ---HWPFGWFLCKLFTIVDINLFGSVFLIALDRICVCLHPVMTQNHRTVSLAKKVI 117
Qy 147 VGPWILALVTLPLVFLFTVTPNPGDITYCTFNFAWSGCTPEERLKVATMLTARGIIRF 206
Db 118 IGPWALLTLPLVIRVTIVPGKTGVACTFNFSPTNDPKERINAVAMLTVRGIIRF 177
Qy 207 VIGFSLPMSIVAICYGLIAAKIHKGMKSSRLRVLTAVASFFCWPFPQVALLGV 266
Db 178 IIGFSAFMSIVAVSGVGLATKI-----IKSSRLRVLVSFAAFLCNSFYQVVALIATV 232
Qy 267 WUKEMLFYGYKYKIIDLIVNPTSLAFNSCLNPLMVLVFGQDFRERLIHSLPTSLERALS 326
Db 233 RIRELL-QCMYKEIGIAVDVTSIAIAFFNSCLNP-LYVFMGQDFRERLIHALPASLERALT 290
Qy 327 EDSAPTNDTAANSASPPAETELQA 350
Db 291 EDSTQTSATNTSLPSAEVALQA 314
RESULT 5
PCT-US93-08528-34
; Sequence 34, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-34

Query Match

61.5%; Score 1117; DB 5; Length 315;

Best Local Similarity 67.3%; Pred: No. 1.7e-75;
Matches 218; Conservative 37; Mismatches 59; Indels 10; Gaps 4;

QY 27 ILPLVLGVTVFLVGLVGNGLVWVAGFRMTRTVTTCYLNALADFSTATPLPLIYSMA 86
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |
Db 1 IITYLVFAVRFVLVGLVGNGLVWVAGFRMHTVTTSYLNLAADFSTSLPFFMVLG 60
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 87 MGKEWPGFELCKLIHLVVDINLFGSVFLGFIAGLDCRCICVLHPVWQNHRTVSLAKVI 146
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |
Db 61 ---HWPEGFWLCKFLFTIVDINLFGSVFLIALIALDRVCVCLHPVWQNHRTVSLAKVI 117
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 147 VGPWIALVLTLPLVFLPLTVTTPNGDTYCTFNFASNGCTPEERLKYAITMLTARGIIRF 206
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |
Db 118 IGPWVWALLTLPLVIRKVTIVPGKTVGTVACTFNFSPMTNDPKERINAVAMLTVRGIIRF 177
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 207 VIGFSLPMSIVAICYGLIAAKIHKMGKISSRPLRVLTAVVASFFICWFPPOLVALLGTV 266
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |
Db 178 IIGFSAPMSIVASYGLIAYKI-----IKSRPLRVLSFVAAAFELCWSPQVVALTATV 232
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 267 WLKEMLPYGYKKIIDILVNPTSSLAFFNSCLNPLMYVFGODFRERLIHSLPTSLEIALS 326
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |
Db 233 RIRELL-QGMKEIGIADVTSALAFNSCLNP-LYVFMGQDFRERLIHALPASLERALT 290
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 327 EDSAPTNDTAANSAPPAETELQA 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |
Db 291 EDSTQSDTATNSTPLSAEVALQA 314
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

RESULT 6
US-08-513-9748-348
; Sequence 348, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994


```
; APPLICATION NUMBER: US/08/458.970A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09234
; FILING DATE: 16 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-970A-9

Query Match      28.2%; Score 513; DB 2; Length 350;
Best Local Similarity 33.6%; Pred. No. 7.3e-31;
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

QY 4 NFSTP-LNEYEE-----VSYESAGYTVLRILPVLVGVTFVGLVGNGLVIWVAGF 53
DB 5 NYTTPDGHYDDKDTLDLNTPDVKTNTLRVPDILALVIFAVFVGLVGNALVWVWTA 64
QY 54 RMTRVTTICYNLALADFSFATLPELIVSNAMGEKWPFGWFLCKLIHIVVDINLFG 113
DB 65 EAKRTINAIWFLNLAADFSLCLPILFTSIQHHHPFPGAACSIILPSLILLNMYAS 124
QY 114 FLIGTALDRCTICVLHPVMAQNHRTVSLAMKVIVGFWILALVTLPLVFLFTVTPNGD 173
DB 125 LLLATISADRELLVFKPIWCQNFRCAGLAWIACAVAGLALLTTPSFLYRVV-----RE 179
QY 174 TY-----CTFNFASWGTPPEERLKVATMLTARIIIRFVIGFSIPMSIVAICYGLIAAK 227
DB 180 EYFPKVLICGVGYSH-----DKRRERAV-----AIVRLVGLFGLPPLTLTICYTFILLR 228
QY 228 IHKGMKISSRPLRVLTAVASFFCWFQFQVALLGTWVKEMLFYGYKIIDIIVNPT 287
DB 229 TWSRRATSTKLVVAVASFFFLFWLPYQVTGM-----MSFLEPSSFTLLNKL 281
QY 288 SSL-----AFFNSCLNPMLYVFGQDFRERLIHSLPTSLSRALSEDA-----PTND 334
DB 282 DSLCVSFAYINCCINPIYVAGQGFQGLRKLKSLPLSLRNVLTEESVYVRESKSFTRSTVD 341
QY 335 TAA 337
DB 342 TMA 344

RESULT 8
US-08-876-874-2
; Sequence 2, Application US/08876874
; Patent No. 5942405
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert
; APPLICANT: Bergsma, Dark
; APPLICANT: Foley, James
; APPLICANT: Kumar, Chandrika
; APPLICANT: Sarau, Henry
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING
; METHODS USING C3A RECEPTOR AND C3A
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
```

```
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876.874
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,627
; FILING DATE: 16-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 482 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-876-874-2

Query Match      28.0%; Score 508.5; DB 2; Length 482;
Best Local Similarity 26.6%; Pred. No. 2.2e-30;
Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 EN-----FSTPLNEYEEVSYESAGYTVLRILPVLVGVTFVGLVGNGLVIWVAGFRWTR 57
DB 7 ENSTDLISQWNEPPV-----ILSMVILSLFTLLGPGNGLVWVAGLKMQR 54
QY 58 TTTTCYLMALADFSFATLPLFIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117
DB 55 TWTNFWLHLTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSLIIVLNFASFVLLT 114
QY 118 FTALDRCTICVLHPVMAQNHRTVSLAMKVIVGFWILALVTLPLVFLFTVTPNGDYCT 177
DB 115 AISLDRCLVYFKPIWCQNHRTVGMACISGCIWVAVCMCIPVYVYREIFTDNHNR-CG 173
QY 178 ENFA-----SW-----183
DB 174 YKFGLSLLDYPDFYGDPLNRSLENIIVQPGEMNDRLDPSSFQTNHFWPTVTFQPT 233
QY 184 -----GGTPEE-----R 190
DB 234 FQPSADSLPGSARLTSQLYSNVEKPADVVPKIPSPGFPFIEDHETSPLDNSDAFLSTH 293
QY 191 LKV-----AITMLTARGIRFIRFVIGSLPMSIYA 218
DB 294 LKLPFSASSNSFESELPQGFQDYNNLQGTDDQVPTPLVAITITRLVVGFLPLSVMI 353
QY 219 ICYGLIAAKIHKGMKIS-SRPLRVLTAVASFFCWFQFQVALLGTWVKEMLFYGY 277
DB 354 ACYSFIVFRMQRGFAKSQSKTFRVAVVAVFLVCWTFYHI-----F 396
QY 278 KIIDILVNPTS-----SLAPFNSCLNPMLYVFGQDFRERLIHSLPTSLSLER 323
DB 397 GVLSTLTPTPLGKTLMSWDHVCIALASANSCLNPFYALLGKDFRKAROSIOGILEA 456
QY 324 ALSD-----SAPTNDTANSAS 341
DB 457 AFSEELTRSTHCPSCNNVISERN 479

RESULT 9
```


Db 254 AFALCWGPHYFSLLEAHANPGLRPLVWRG-----LPTVTSIAFFNSVANPVLV 305
Qy 304 FVGQDFRRLHSLPTSLERALSSEDS-----APTNDTAANSASPPA 344
Db 306 LTCPDMRLKRLSRRTVLESVLVDSDSELGGAGSSRRRTSTARSASPLA 355

RESULT 11

US-08-118-270-35
; Sequence 35, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-08-118-270-35

Query Match 26.4%; Score 479; DB 1; Length 304;
Best Local Similarity 33.8%; Pred. No. 2.1e-28;
Matches 112; Conservative 56; Mismatches 109; Indels 54; Gaps 9;
Qy 27 ILPLVLGVGTFVLGVLGNLVIWVAGFRMTRVTTTCYLNALADFSFATLPFLIVSMA 86
Db 2 ILALVFAVVLGVGLGNLVIWVTAFAEKRTINAIWFLNIWADFLSCLALPILFTSIV 61
Qy 87 MGEKPPGFQWFLCKLHIWVDINLFGSVFLIGFIADRCICVLHPVWQNHRTVSLAMKVI 146
Db 62 QHHHPFGGAACSLPSILLNMYASILLATISADRFLLVFKPIWQCNFRGAGLAWIAC 121
Qy 147 VGPWILALVLPVLELTFTVTPNGDTY-----CTENFASWGCTPEERLKVATMLTA 200
Db 122 AVANGIALLLTIPSLYRW-----REYFPKVLGGQDYSH-----DKRRERAV----- 166
Qy 201 RGIIRFVIGFSLPMSIAICYGLIAAKIHKGMKISSRPLRVLTAVAVASFFFCWPPFQLV 260
Db 167 -AIVRLVGLFWLPLTLTICY-----TTSTKTLKVVAVAVASFFFIWLPYQVT 214

Qy 261 ALLGTVWLKEMLFYGYKIIDLIVNPTSSL-----AFFNSCLNPMLYVFGQ-DFRERLIH 315
Db 215 GIM-----MSFLPSSPTFLLLKLDLSLCVFSYAINCCINPIIYVWAGQGFQGRLRK 267
Qy 316 SLPTSLERALSSEDS-----PTNDTAA 337
Db 268 SLPSLLRNVLTEESVVRKSKSFSTRSTVDTMA 298

RESULT 12

PCT-US93-08528-35
; Sequence 35, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-35

Query Match 26.4%; Score 479; DB 5; Length 304;
Best Local Similarity 33.8%; Pred. No. 2.1e-28;
Matches 112; Conservative 56; Mismatches 109; Indels 54; Gaps 9;
Qy 27 ILPLVLGVGTFVLGVLGNLVIWVAGFRMTRVTTTCYLNALADFSFATLPFLIVSMA 86
Db 2 ILALVFAVVLGVGLGNLVIWVTAFAEKRTINAIWFLNIWADFLSCLALPILFTSIV 61
Qy 87 MGEKPPGFQWFLCKLHIWVDINLFGSVFLIGFIADRCICVLHPVWQNHRTVSLAMKVI 146
Db 62 QHHHPFGGAACSLPSILLNMYASILLATISADRFLLVFKPIWQCNFRGAGLAWIAC 121
Qy 147 VGPWILALVLPVLELTFTVTPNGDTY-----CTENFASWGCTPEERLKVATMLTA 200
Db 122 AVANGIALLLTIPSLYRW-----REYFPKVLGGQDYSH-----DKRRERAV----- 166
Qy 201 RGIIRFVIGFSLPMSIAICYGLIAAKIHKGMKISSRPLRVLTAVAVASFFFCWPPFQLV 260
Db 167 -AIVRLVGLFWLPLTLTICY-----TTSTKTLKVVAVAVASFFFIWLPYQVT 214
Qy 261 ALLGTVWLKEMLFYGYKIIDLIVNPTSSL-----AFFNSCLNPMLYVFGQ-DFRERLIH 315

Db 215 GTM-----MFLEPSSPTFLLLKLDLCVSPAYINCINPIIYVAGQFQGRKK 267
QY 316 SLPTSIALSESDA-----PTNDTAA 337
Db 268 SLPSLLRNVLTEESVVRKSKFTSRSTVDMA 298

RESULT 13
US-08-513-974B-349
; Sequence 349, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.

; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-349

Query Match 25.5%; Score 464; DB 3; Length 124;
Best Local Similarity 69.4%; Pred. No. 1.1e-27;
Matches 86; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 125 ICVLHPVWQNHRTVSLAMKVIVGWPWILALVLTLPVFLFTVTTPNGDTYCTFNFSWG 184
Db 1 VCVLHPVWQNHRTVSLAKKVIIGPWVWALLTLTPVIRVTTPVPGKTGTACTFNFSWPT 60
QY 185 GTPERLKVAITMLTARGIIRVIGFSLPMSIVAICYGLIAAKHKMGKSRPLRLVT 244
Db 61 NDPKERIKVAVAMLVIRGIIRFIIGFSAPMSIVAVSYGLIATRIKHQGLIKSRPLRLVLS 120
QY 245 AYVA 248
Db 121 FVA 124

RESULT 14
US-08-513-974B-350
; Sequence 350, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995

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